

1 10 20 30 40 50 60 70 80 90 100
 human MRPQGPAAAPQRLRGL--LLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNGMCLQGPAGVPGROGSPGANGIPGTPGIPGRDGFKEKGECLRESF
 mouse MHPQGRAAPPQLLGLFLVLLLLQLSAPSSASENPKVKQKALIRQREVVDLYNGMCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKEKGECLRESF
 rice_fish MTPLSPRLILLCLALPLHGQE--KGRSRGYRKDPDADKF--GSCLOGPAGTPGRDGNPGANGIPGTPGIPGRDGLKGEKGEVCVSEVF
 abra_fish MGTKLTQLLLICFWISLPCVTVQKAKERIPRQ-RDAEFTDKYA-CVQGVPGVQGRDGNPGINGIPGTPGIPGRDGLKGEKGEVCVSEVF
 chicken RPREVLEAYNGVCLQGPSVPGRDGNPGTNGIPGTPGIPGRDGNPG.GvpgRDGNPG.NGIPGTPGIPGRDG.KGEKGECLRESF
 nsensusll.....p.....k.....r.r#v...yng.CLQGP.GvpgRDGNPG.NGIPGTPGIPGRDG.KGEKGECLRESF
 101 110 120 130 140 150 160 170 180 190 200
 human EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYFTFNAGACSGPLPIEAIYYLDQGSPELNNSTINIHRTSSVE
 mouse EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYFTFNAGACSGPLPIEAIYYLDQGSPELNNSTINIHRTSSVE
 rice_fish EEPWKPNYKQCAWNSLYGIDLGKIACTFTKLRSEALRVLFSGSLRLKCKEACCQRWYFTFDGAECTGPLPVESIIYLNQGSPELNNSTINIHRTSSVE
 abra_fish EEPWKPNYKQCAWNSLYGIDLGKIACTFTKQSDSALRVLFSGSLRLKCKTACCQRWYFTFNAGAECTGPLPIESIVYLDQGSPELNNSTINIHRTSTVE
 chicken EESWTPNYKQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRSACCQRWYFTFNAGACAGPLPIEAIYYLDQGSPELNNSTINIHRTSSVE
 nsensus EESWTPN%KQCSWSSLYGIDLGKIA#CTFTKRS#SALRVLFSGSLRLKCr.ACCQRWYFTF#GAEC.GPLP!EaI!YL#QGSPE\$NSTINIHRTSSVE

FIG.-1

201 210 220 230 240 245
 human GLCEGIGAGLVDAIWVGTCSDPKGDASTGWNVSRIIEELPK
 mouse GLCEGIGAGLVDAIWVGTCSDPKGDASTGWNVSRIIEELPK
 rice_fish GLCEGIGAGLVDAIWVGTCDYPRGDASTGWNVSRIIEELPK
 abra_fish GLCEGIGAGLVDAIWVGTCDYPRGDASTGWNVSRIIEELPK
 chicken GLCEGINAGLVDAIWVGTCSDPKGDASTGWNVSRIIEELPK
 nsensus GLCEGI.AGLVD!aIWVGTCSDPKGDASTGWNVSRIIEELPK

10 20 30 40 50
 MRPQGPAAAPQRLRGLLLLLLLQLPAPSSASEIPKQKQALRQREVVDLYNG
 60 70 80 90 100
 MCLQGPAGVPGRDGSPGANGIPGTPGIPGRDGFKEKGECLRESFESWTPNY
 110 120 130 140 150
 KQCSWSSLYGIDLGKIAECTFTKMRNSALRVLFSGSLRLKCRNACCQRWYF
 50 170 180 190 200 210
 TFNAGACSGPLPIEAIYYLDQGSPELNNSTINIHRTSSVEGLCEGIGAGLVDA
 220 230 240
 IWVGTCSDPKGDASTGWNVSRIIEELPK

FIG.-2

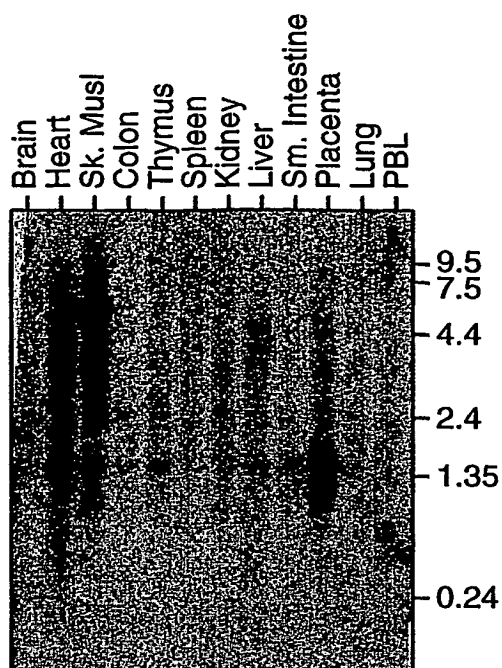


FIG._3A

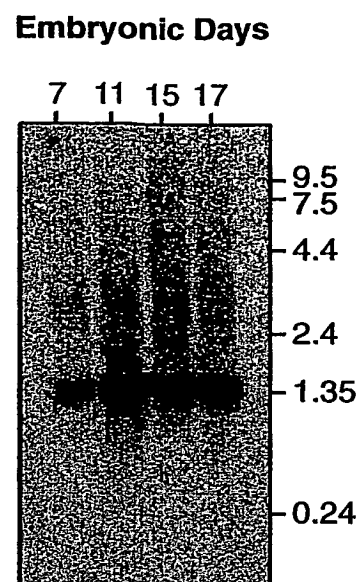


FIG._3B

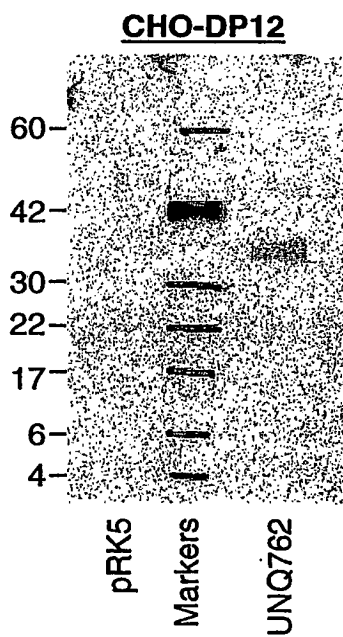


FIG._4A

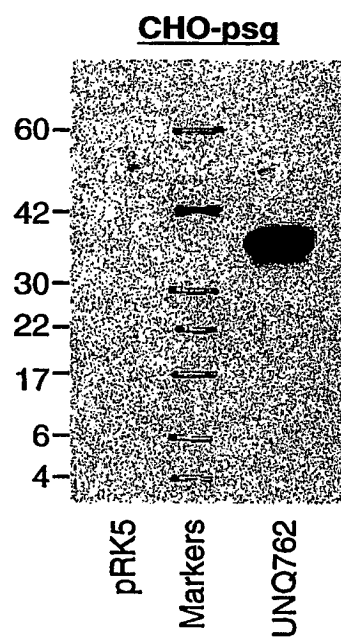
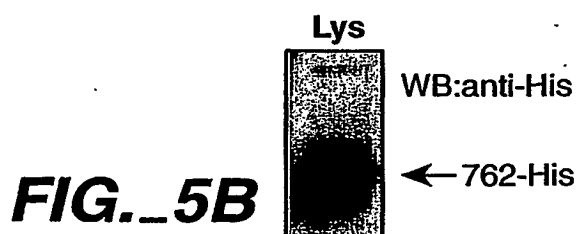
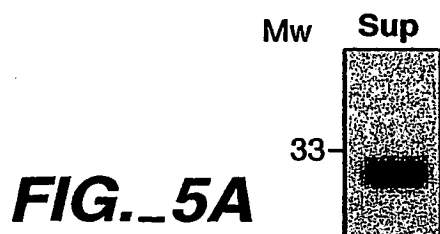


FIG._4B



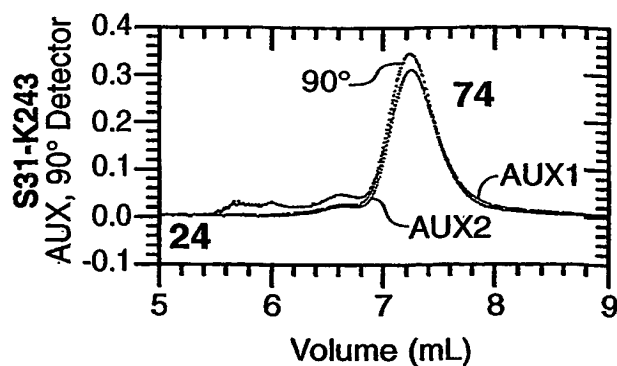


FIG._6A

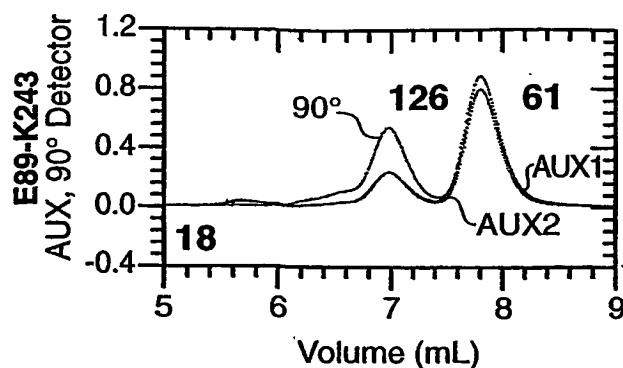


FIG._6B

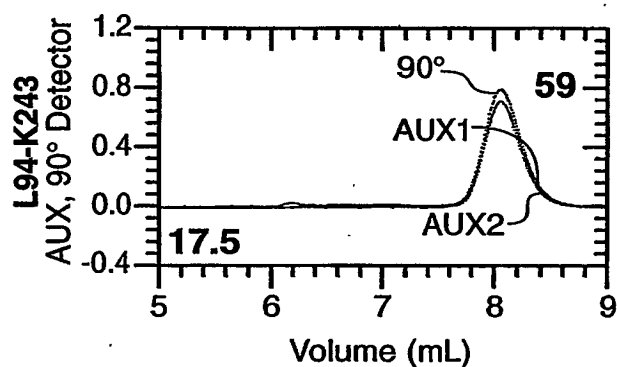


FIG._6C

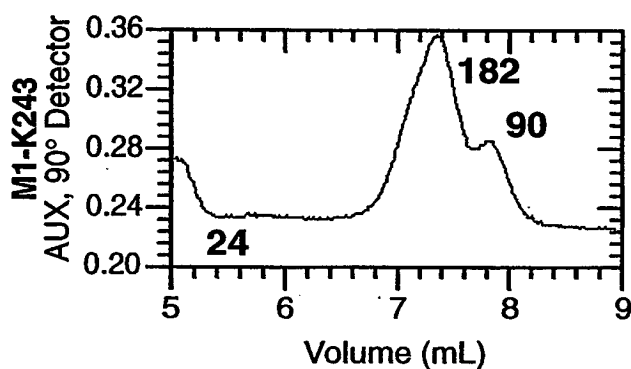


FIG._7A

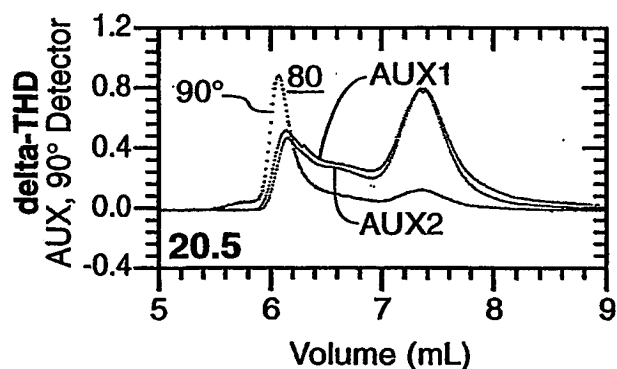


FIG._7B

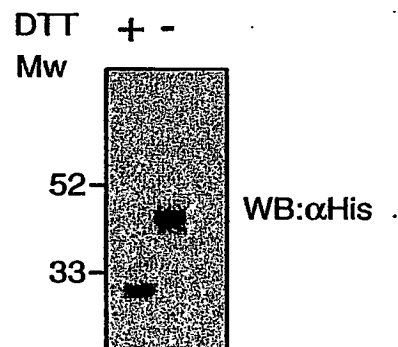


FIG._7C

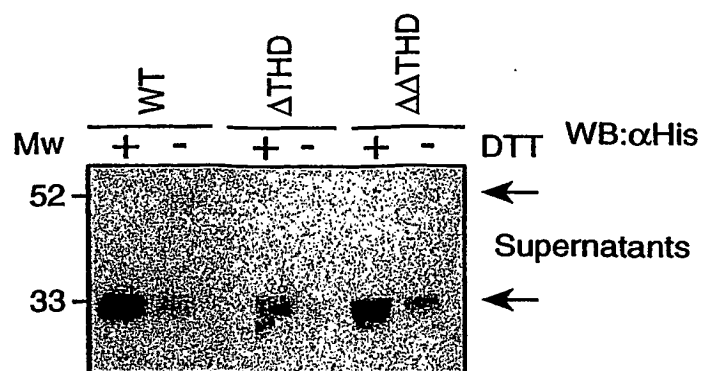
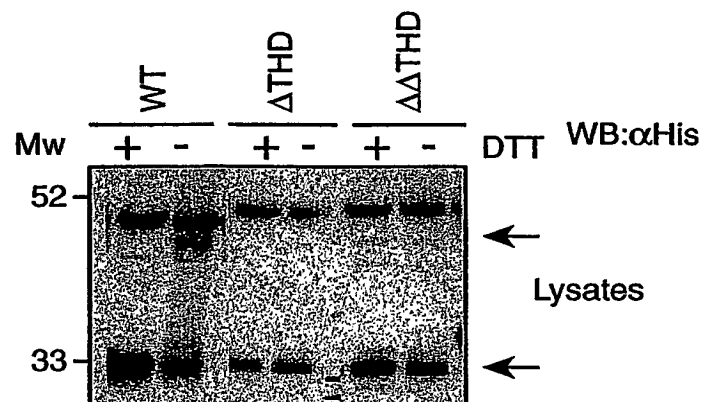
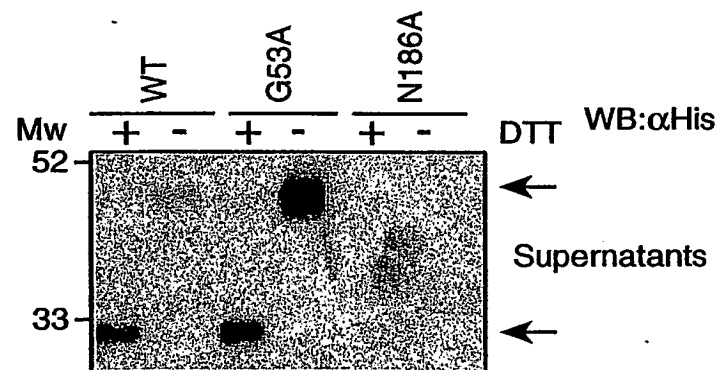
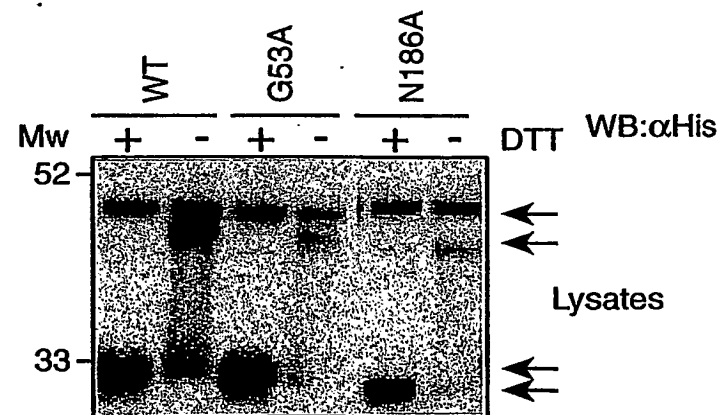
FIG._8A**FIG._8B****FIG._9A****FIG._9B**

FIG._10A

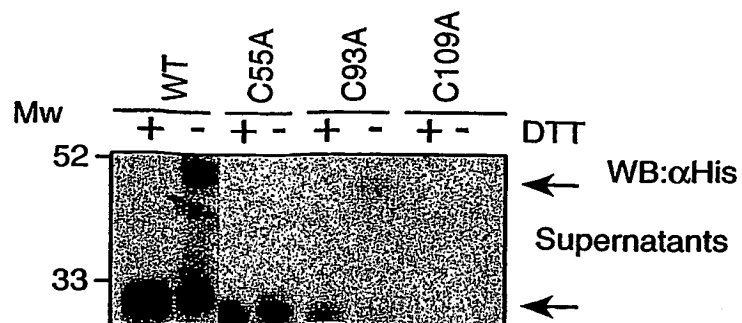


FIG._10B

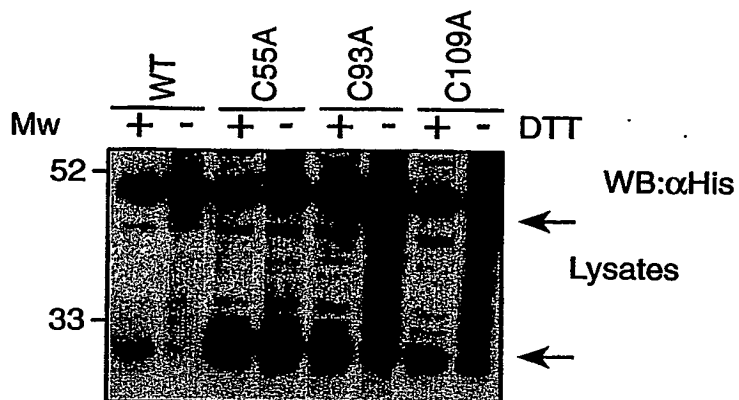
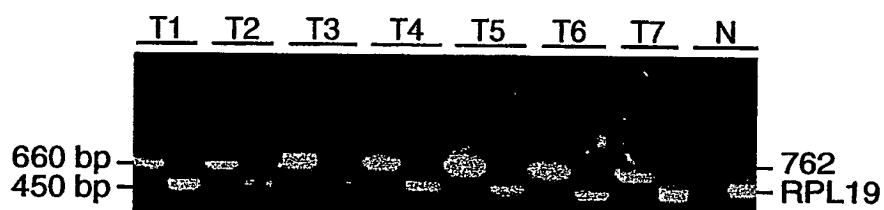
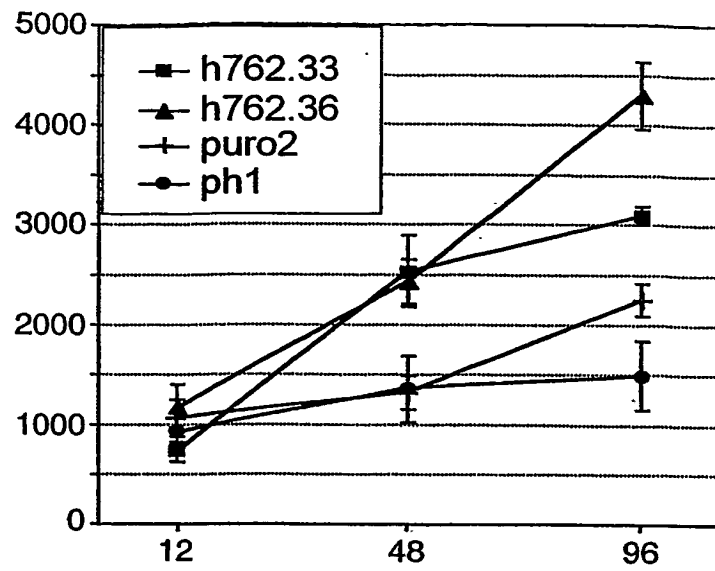
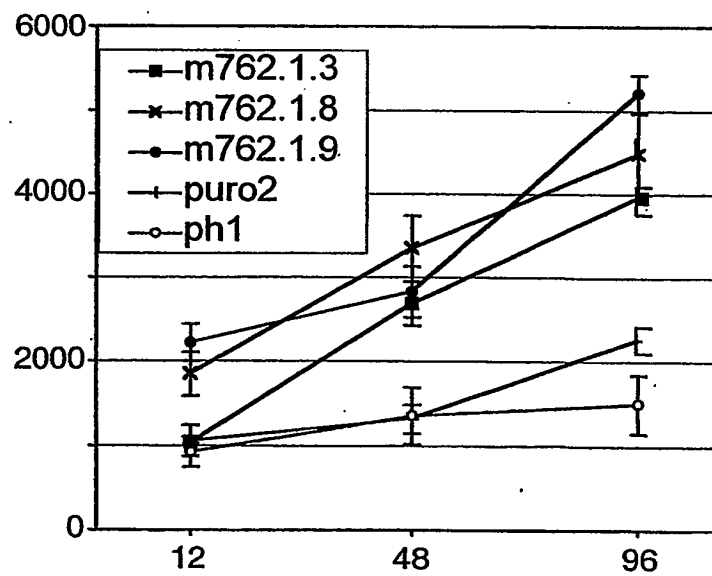


FIG._11



**FIG. 12A****FIG. 12B**

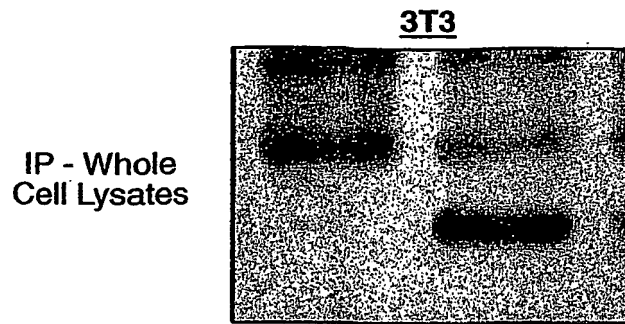


FIG. 13A

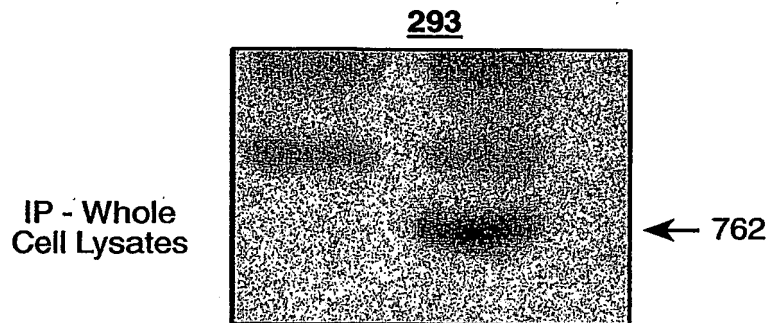


FIG. 13B

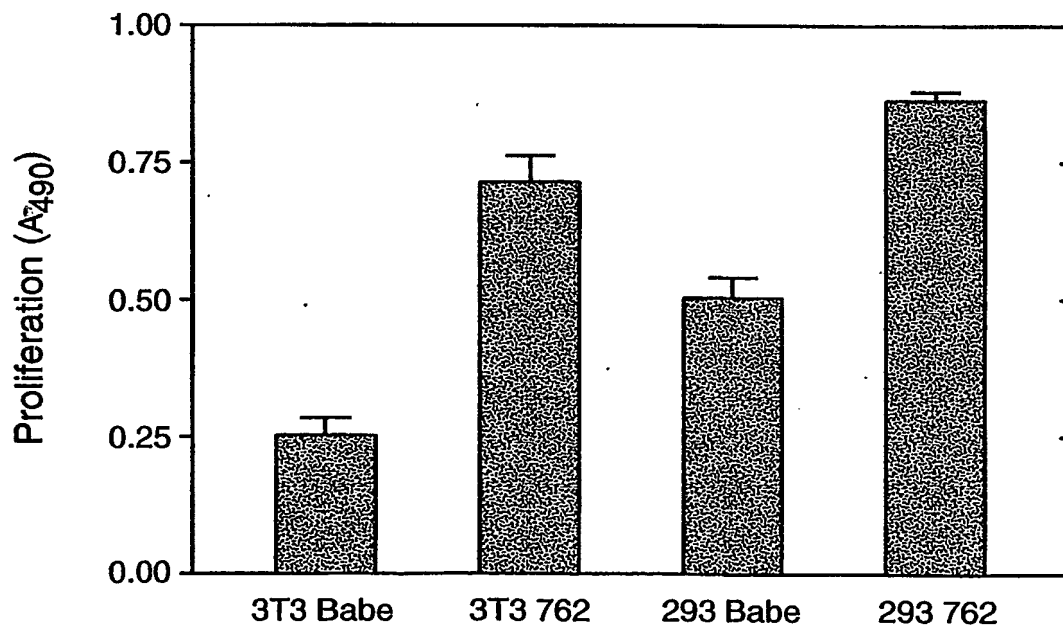


FIG. 13C

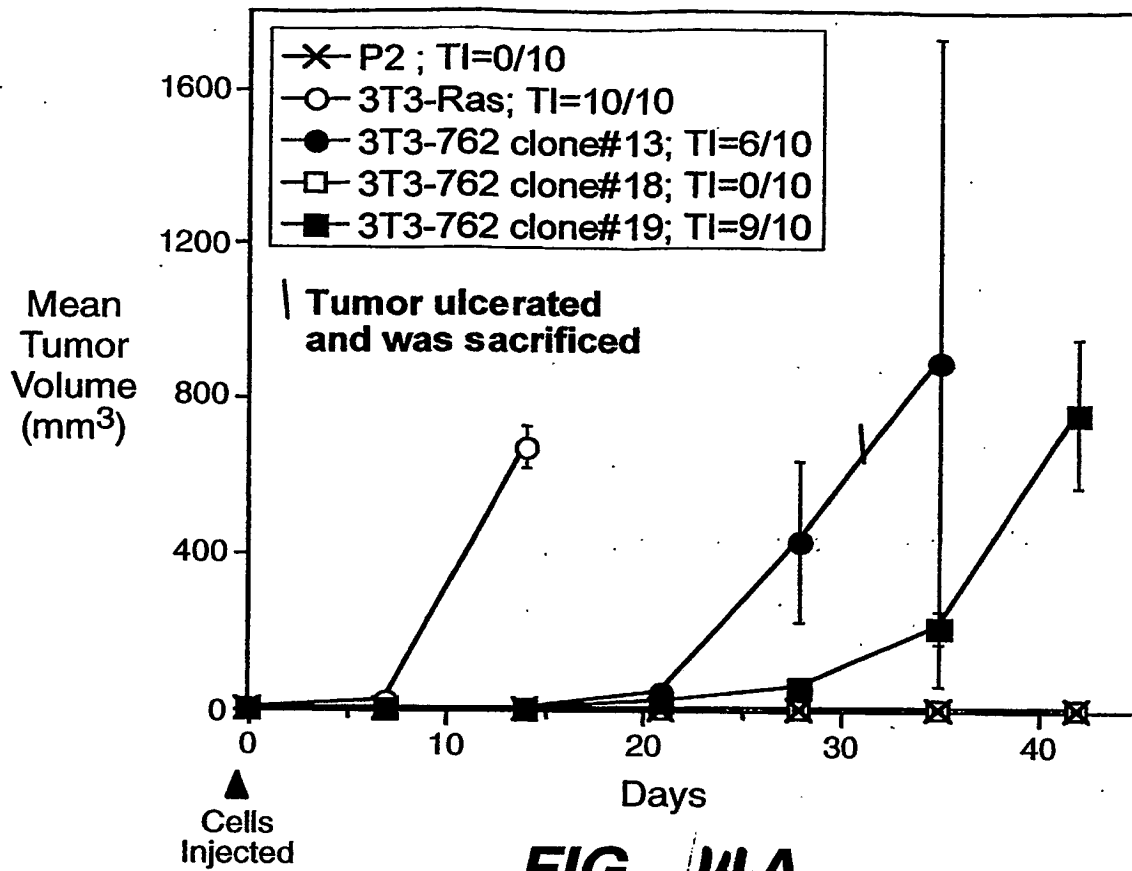


FIG. 14A

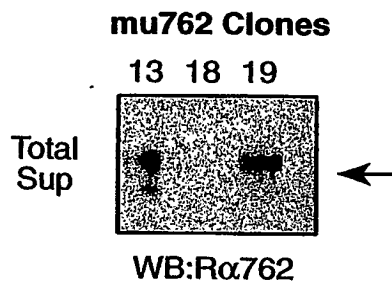


FIG. 14B

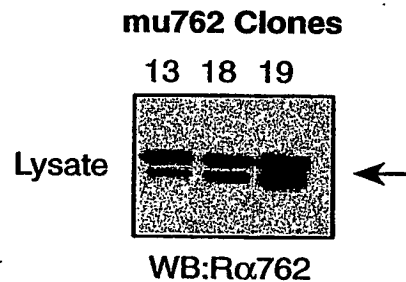
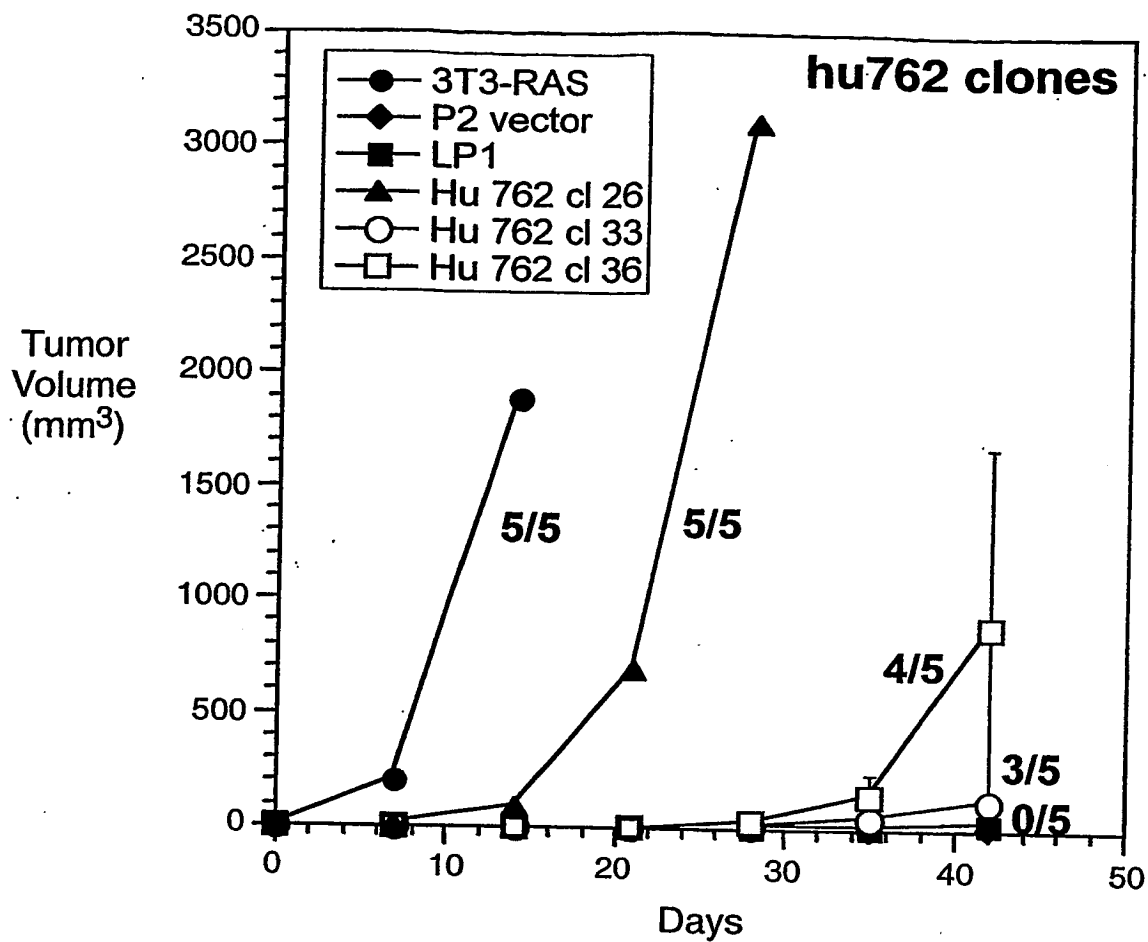


FIG. 14C

**FIG. 15**

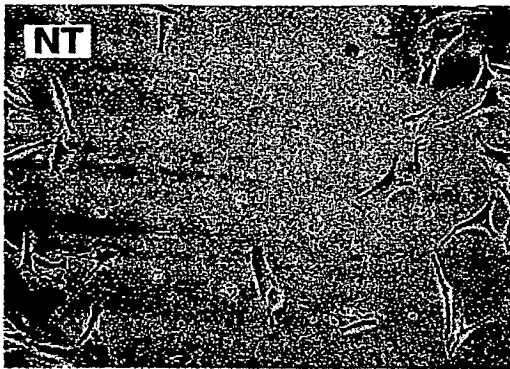


FIG. 16A



FIG. 16C



FIG. 16B



FIG. 16D

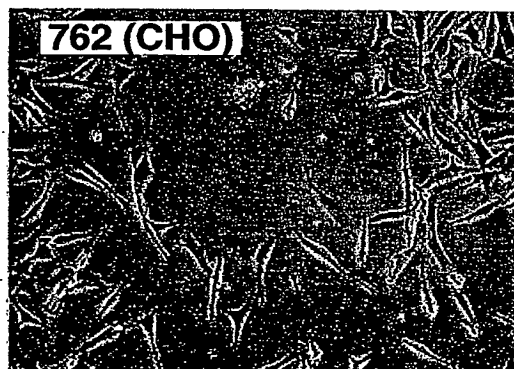
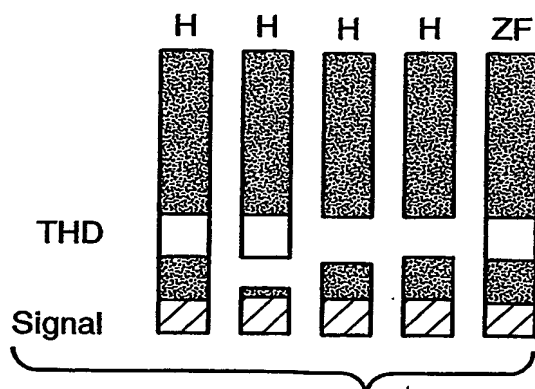
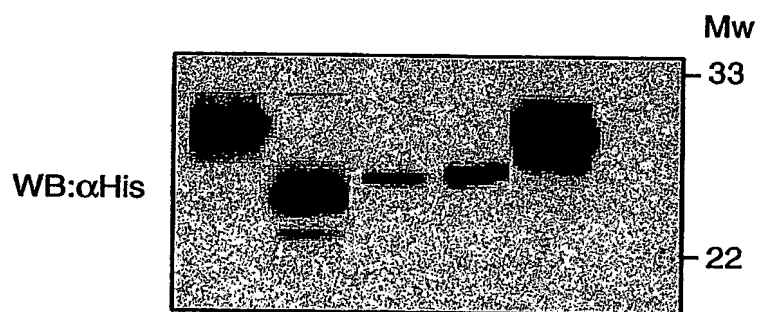
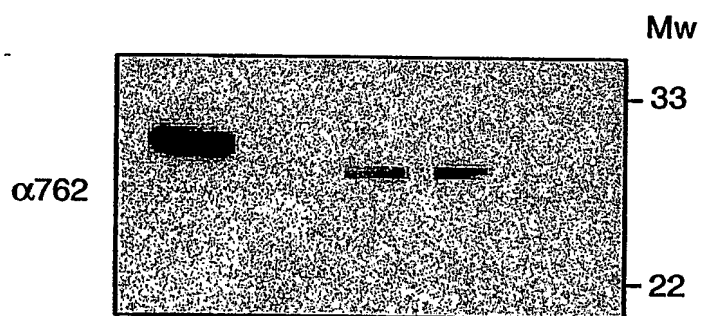


FIG. 16E

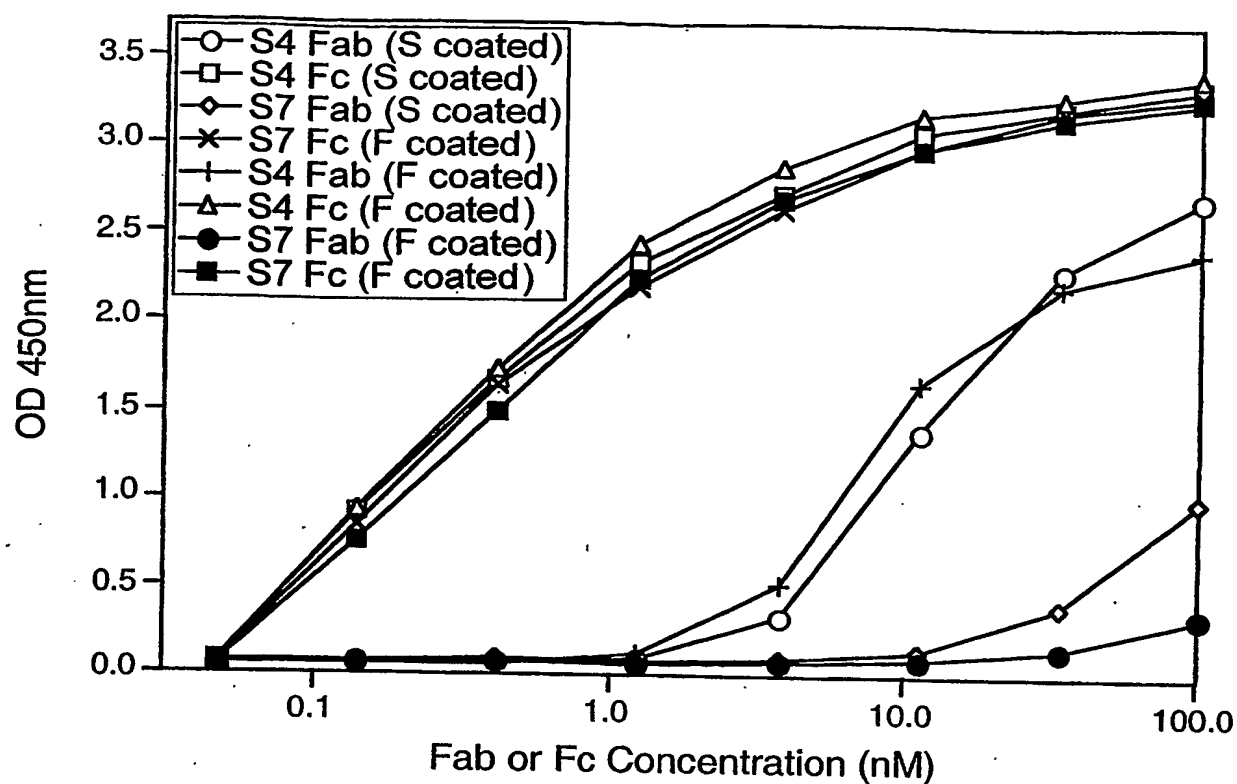
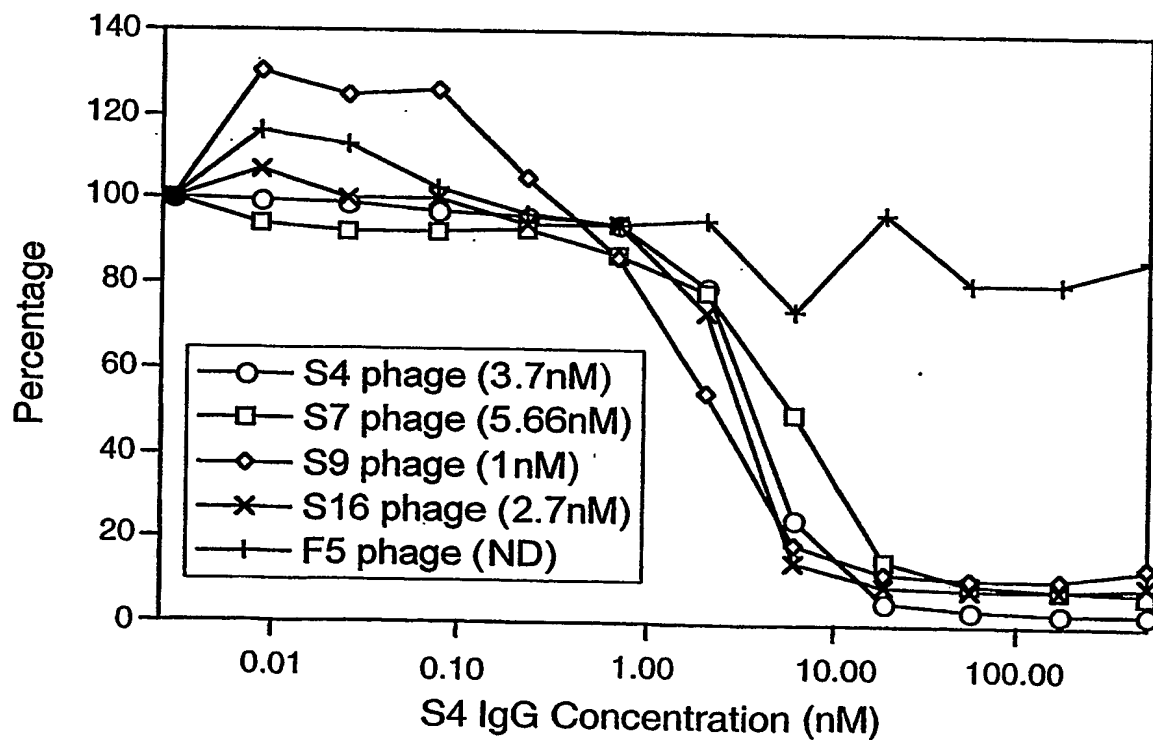
**FIG. 17A****FIG. 17B****FIG. 17C**

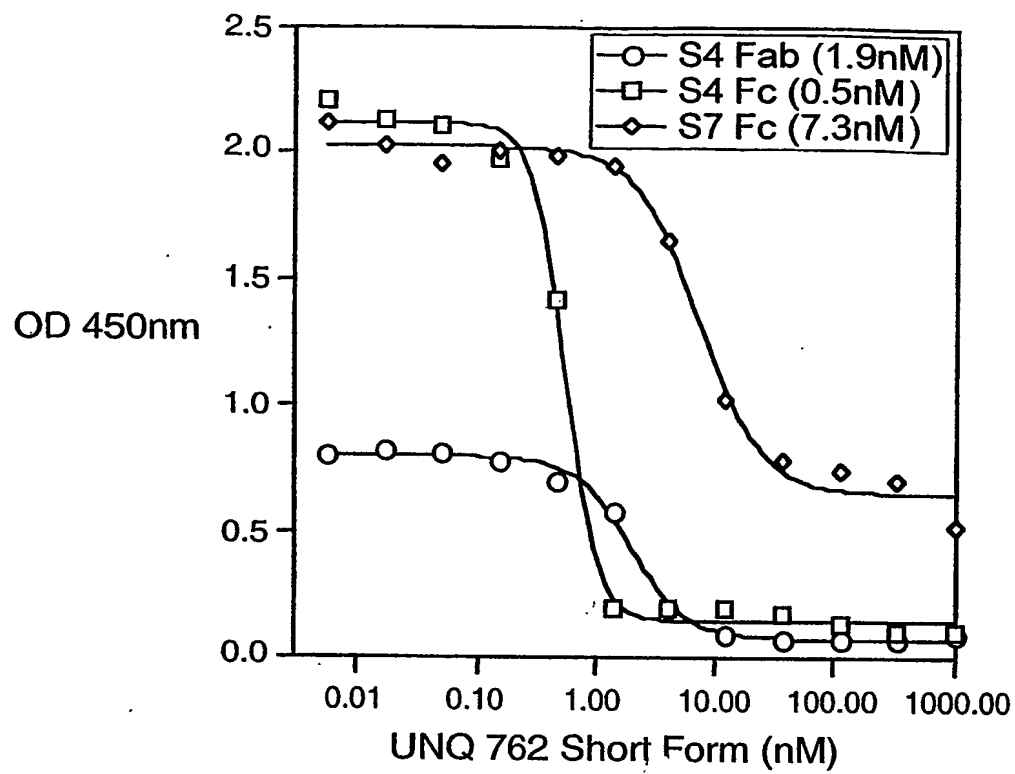
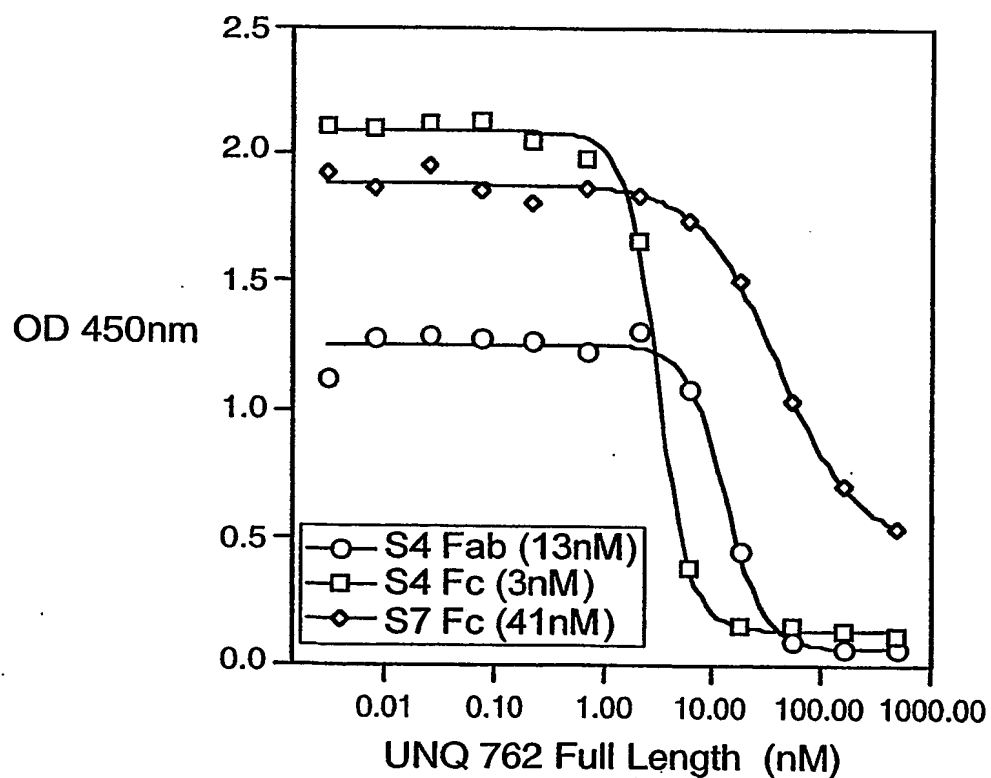
H1										H2										H3										Name	
8	29	30	31	32	33	49	50	51	52	52a	53	54	55	56	57	58	92	93	94	95	96	97	98	99	100	100a	100b	100c	101	102	
I	S	G	S	D	D	G	R	I	S	P	Y	G	G	N	T	N	C	A	R	V	G	G	L	K	L	L	-	F	D	Y	S7
I	T	N	S	D	D	A	T	I	Y	P	Y	G	G	Y	T	Y	C	A	R	G	G	M	D	G	Y	V	M	D	Y	S16	
I	N	N	Y	D	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F5
I	N	N	Y	D	D	G	Y	I	S	P	P	S	G	A	T	Y	C	A	R	M	V	G	M	R	R	G	V	M	D	Y	F6
I	S	G	S	W	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	S4
I	S	N	Y	G	G	G	R	I	S	P	S	N	G	S	T	Y	C	A	K	C	S	V	R	-	-	-	-	F	A	Y	S9
I	S	G	S	W	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F13
I	S	G	S	W	W	A	W	I	A	P	Y	S	G	A	T	D	C	A	R	E	G	G	L	Y	W	V	-	F	D	Y	F47

FIG. 18

Phage			Fab			IgG		
762 S/S	762 F/F		762 S/S	762 F/S	762 F/F	762 S/S	762 F/F	
3nM	0.9nM		3.6nM (1.9nM)	32nM	13.4nM	0.5nM	3.1nM	
762 S/S	762 F/F		762 S/S	762 F/S	762 F/F	762 S/S	762 F/F	
35nM	2.7nM		113nM	57nM	n/a	7.3nM	41nM	
S4								
S7								

FIG. 19

**FIG. 19****FIG. 20**

**FIG. 20 A.****FIG. 20 B.**

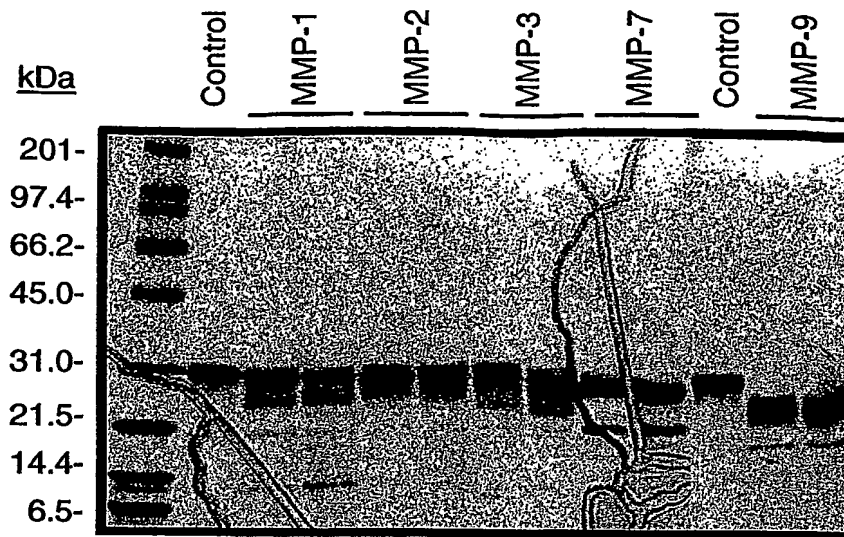


FIG. 23

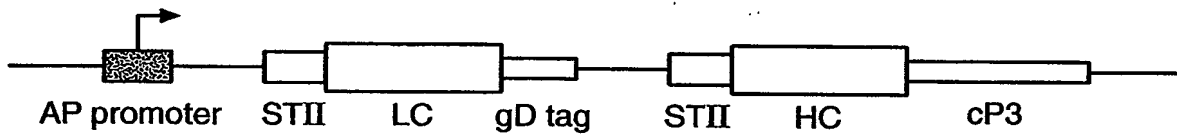


FIG. 24 A

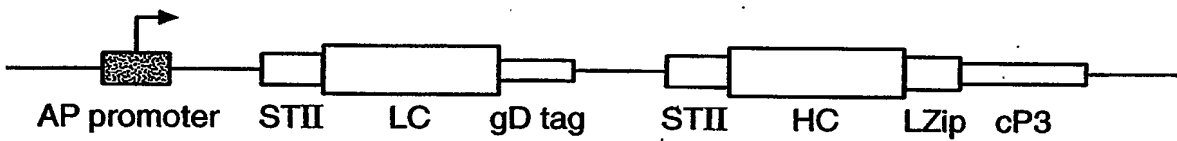


FIG. 24 B

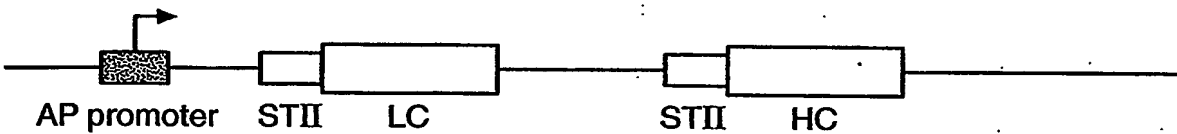


FIG. 24 C

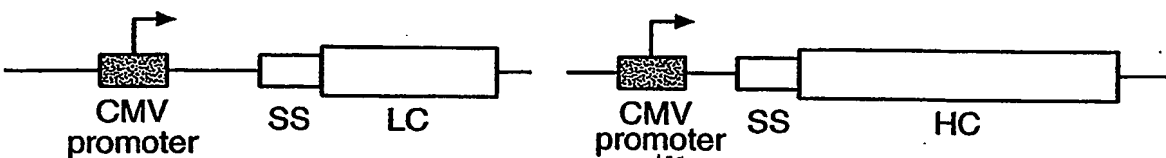


FIG. 24 D

1 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTATTAT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
 CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTTAG AGTAACGACT CAACAATAAA TTGGAACGGG TTTTTCITTTCT TCTCAGCTTA

 101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATATG TCGCAAAATG ACCAACACAGG GTTGATTGAT CAGGTAGAGG
 CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GAGGTACGA AGCGTTATAC CGCGTTTTAC TGGTTGTCGC CAACATACTA GTCCATCTCC

 201 GGGCGCTGTA CGAGGTAAAG CCGGATGCCA GCATTCTGTA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
 CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAGC CGCTAATGCA TTTTCTCAAT AACTTCGTAG GAGCAGTCAT

 301 AAAAGTTAAT CTTTTCACA GCTGTCATAA AGTTGTCAGG GCCGAGACTT ATAGTCGCTT TGTTTTATT TTTTAATGTA TTTGTAACATA GTACGCAAGT
 TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

 401 TCACGTAAAA AGGGTATGTA GAGGTGAGG TGATTTTATG AAAAAGAATA TCGCATTTCT TCTTGCACTT ATGTTCTGTTT TTTTCTATTGC TACAAATGCC
 AGTGCATTTT TCCCATACAT CTCCAACCTCC ACTAAAATAC TTTTTCITAT AGCGTAAAGA AGAAGCTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
 1 M K K N I A F L L A S M F V F S I A T N A
 ^start of stII signal sequence
 ^met

 501 TATGCAGATA TCCAGATGAC CCAGTCCCGG AGCTCCCTGT CGGCTCTGT GGGCGATAGG GTCACCATCA CCTGCCGTGC CAGTCAGGAT GTGTCCACTG
 ATACGTCTAT AGGTCTACTG GGTCAAGGGC TCCAGGGACA GGGGGAGACA CCGGTATCC CAGTGGTAGT GGACGGCAGG GTCAGTCCCTA CACAGGTGAC
 22 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
 ^start of light chain
 ^CDR-L1

 601 CTGTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCCCTCA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
 GACATCGGAC CATAGTTGTC TTTGGTCTCT TTCGAGGCTT CGAAGACTAA ATGAGCGGTA GGAAGGAGAT GAGACCTCAG GGAAGAGCGA AGAGACCATC
 56 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
 ^CDR-L2

 701 CGGTCCGGG ACGGATTICA CTCTGACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTAAGTGT CAGCAATCTT ATACTACTCC TCCCACGTTT
 GCCAAGGCCC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC GTCGGCCTTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGGTGCAAG
 89 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
 ^CDR-L3

FIG.- 25A


```

301 GGACAGGGTA CCAAGGTGGA GATCAAAACGA ACTGTGGGCTG CACCATCTGT CTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCCTCTG
CCTGTCCCAT GGTTCACCT CTAGTTTGCT TGACACCGAC GTGGTAGACA GAAGTAGAAG GCGGTAGAC TACTCTCAA CTTTAGACCT TGACGGAGAC
122 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V

301 TTGTGTGCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGGTGGATA AGCCCTCCA ATCCGGTAAC TCCCAGGAGA GTGTACACAGA
AACACACGGA CGACTTATTG AAGATAGGTT CTCTCCGGTT TCATGTCCACC TTCCACCTAT TCGGGGAGGT TAGCCCATTG AGGCTCTCT CACAGTGTCT
156 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

301 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCTGCCA AGTCACCCAT
CGTCCTGTG TCCCTGTGCT GGATGTCGGA GTCTGCTGG GACTGCGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGGACGCT TCAGTGGGTA
89 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H

301 CAGGECCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCCGCGGT AAGGACCTGG
GTCCCGGACT CGAGCGGGCA GTGTTTCTCG AAGTTGTCCC CTCTCACACC ACGTTCGAGG CCATACCGAC TAGGCTTGGC AAAGCGCCA TTCTGGGACC
222 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A

301 CATAACTCGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTAGC CAAGTTCAG TAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
GTATTGAGCT CCGACTAGGA GATCGGCGCT GCGTAGCACC GGGATCATGC GTTCAAGTGC ATTTTTCCTCA TTGATCTCCA ACTCCACTAA AATACTTTT
56 O

301 GAATATCGA TTTCTTCTTG CATCTATGTT CGTTTTTCT ATTGCTACAA ACGGTACGC TGAGGTTCAG CTGTGGAGT CTGGCGGTGG CCTGGTGCAG
CTTATAGCGT AAAGAAGAAC GTAGATACAA GCAGGAGGTA TAACGATGTT TGCGCATGCG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACCACTGC
20 N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V Q

301 CCAGGGGGCT CACTCCGTTT GTCTGTGCA GCTTCTGGCT TCAACATTAA AGACACCTAT ATACACTGG TCGTTCAGC CCGGGTAAG GGCCTGGAAT
GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTTGTAATT TCTGTGGATA TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
14 P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E W

301 CDR-H1

```

M K K
^start of stII

^start of heavy chain

FIG. 25B

1501 GGGTTGCAAG GATTTATCCT AGGAATGGTT ATAATAGATA TGCCGATAGC GTCAAGGGCC GTTTCACAT AAGCGCAGAC ACATCCAAA ACACAGCCTA
 CCCAACGTTT CTAATAGGA TGCTTACCAG TGCTTACCAG CAGTTCCCG CAAAGTGATA TTCCGGCTCTG TGTAGGTTTT TGTGTCGGAT
 48 V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A Y
 ^CDR-H2
 1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATATATTGA GCCGCTGGGG AGGGACGGC TTCTATGCTA TGGACTACTG GGTCAAGGA
 GGATGTTTAC TTGTCCGAAT CTGCACTCCT GTGACGGCAG ATAATAACAT CGCGACCCC TCCCCTGGG AAGATACGAT ACCTGATGAC CCCAGTTCTT
 81 L Q - M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q G
 ^CDR-H3
 1701 AACTAGTCA CCGTCTCCTC GGCCTCCACC AAGGGCCCAT CCGTCTTCCC CTTGGCACCC TCCTCCAAGA GCACCTCTGG GGCACACGG GCCCTGGGCT
 TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA GCCAGAAGG GACCGTGGG AGGAGTTCT CTGTGGAGACC CCCGTGTGCG CGGGACCCGA
 114 T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C
 1801 GCCTGGTCAA GGACTACTTC CCGAACCAGG TGACGGTGC GTGGAACCTA GCGGCCCTGA CCAGCGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCT
 CGGACCAGTT CCTGATGAG GGGCTTGGCC ACTGCCACAG CACCTTGAGT CCGCGGGACT GGTCCCGCA CGTGTGGAAG GCGCAGACAG ATGTCAGGAG
 148 L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S
 1901 AGGACTCTAC TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC AACCTGAATC ACAAGCCAG CAACACCAAG
 TCCTGAGATG AGGAGTCGT CGCACCCTG GCACGGGAGG TCGTCAACC CGTGGTCTG GATGTAGACG TTGCACTTAG TGTTCGGTC GTTGTGTTTC
 181 G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K
 2001 GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAATC ACCTCAGTGG CCGTGGCTCT GTTCCGGTG ATTTTGATTA TGAAGAAGATG GCAAACGCTA
 CAGCTGTCTT TTCAACTCGG GTTTAGAACA CTGTTTGTAG TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAACCTAAT ACTTTCTAC CGTTTGGGAT
 214 V D K K V E P K S C D K T H L S G G S G S G D F D Y E K M A N A N
 ^end of heavy chain
 ^start of gene III coat protein (267-end)
 2101 ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCT ACAGCTGAC GCTAAAGGA AACTTGATTC TGTCGCTACT GATTACGGTG CTGCTATCGA
 TATTCCCCG ATACTGGCTT TTACGGCTAC TTTTGGCGGA TGTCAGACTG CGATTTCCGT TTGAACCTAG ACAGCGATGA CTAATGCCAC GACGATAGCT
 248 K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G A A I D

FIG. 25c

2201 TGGTTTCAATT GGTGACGTTT CCGGCCCTTGC TAATGGTAAT GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAATAGG CTCAAAGTCGG TGACGGTGTAT
 ACCAAAGTAA CCACTGCAAA GGCCGGAACG ATTACCATTA CCACGATGAC CACTAAACG ACOGAGATTA AGGTTTACC GAGTTACGCC ACTGCCACTA
 281 G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G D G D
 2301 AATTCACCTT TAATGAATAA TTTCCTGTCAT TATTACCTT CCCTCCCTCA ATCGGTGAA TGTCGCCCTT TTGTCTTTAG CGTGGGTAAA CCATATGAAT
 TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA GGGAGGAGT TAGCCAACCT ACAGCGGAA AACAGAAATC GCGACCATTT GGTATFACTA
 314 N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K P Y E F
 2401 TTCTCTATGA TTGTGACAAA ATAAACTTAT TCCGTGGTGT CTTTGGCTTT CTTTATATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT
 AAAGATAACT AACACTGTTT TATTGTAATA AGGCACCACA GAACGCAAA GAAATATATAC AACGCTGGAA ATACATACAT AAAAGATGCA AACGATTTGA
 348 S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T F A N I
 2501 ACTGCGTAAT AAGAGTCTT AATCATGCA GTTCTTTTGG CTAGCGCCG CCFATACCTT GTCTGCCTCC CCGCGTTGG TCGCGGTGCA TGGAGCCGGG
 TGACGCATTA TTCTCAGAA TTAGTACGGT CAAGAAAACC GATCGCGCG GATATGGAA CAGACGGAGG GCGCAACGC AGCGCCACGT ACCTCGGGCC
 381 L R N K E S O
 2601 CCACCTCGAC CTGAATGGAA GCCGGCGGCA CCTCGCTAAC GGATTCACCA CTCCAAGAAT TGGAGCCAAT CAATTCTTGC GGAGAACTGT GAATGGCGAA
 GGTGGAGTGT GACTTACCTT CGGCGGCCGT GGAGCGATTG CCTAAGTGGT GAGGTTCTTA ACCTCGGTTA GTTAAGAAGC CTTCTTGACA CTTACGGCTT
 2701 ACCAACCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT CCAGCAGCG CAGCGGGCG ATCTCGGCA GCGTTGGGT CTTGCCACCG GTGCCGATGA
 TGGTTGGGA CCGTCTTGTA TAGGTAGCG AGGCGGTAGA GGTCTGTGGC GTGCGCCGCG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACCGCTACT
 2801 TCGTCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGG TTGCCTTACT GGTTAGCAGA ATGAATCACC GATACGCGAG CGAACGTGAA GCGACTGCTG
 AGCAGGAGA CAGCAACTCC TGGGCCGATC CGACCGCCC AACGGAATGA CCAATGCTCT TACTTAGTGG CTATGCGCTC GCTTGACCTT CGCTGACGAC
 2901 CTGCAAAACG TCTGCGACCT GAGCAACAC ATGAATGGTC TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA ACGCGGAAGT CAGCGCCCTG CACCATATG
 GACGTTTTCG AGACGCTGGA CTCGTTGTTG TACTTACCAG AAGCCTAAGG CACAAAGCAT TTCAGACCTT TCGCCCTTCA GTCGCGGAC GTGGTAATAC
 3001 TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTG GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGAAT TTTCTCTGTT
 AAGGCCTAGA CGTAGCGTCC TAGCAGGACC GATGGGACAC CTTGTGGATG TAGACATAAT TGCTTCGCGA CGTAACTGG GACTCACTAA AAAGAGACCA

FIG. 25D

101 CCGCGCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG TTCCAGTAAC CCGGCATGTT CATCATCAGT AACCGGTATC GTGAGCATCC TCTCTCGTTT
 GGGCGGCGTA GGTATGGCGG TCAACAAATG GGAGTGTTGC AAGGTCAATG GCGGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAAA

 201 CATCGGTATC ATTACCCCA TGAACAGAAA TTCCCCCTTA CACGGAGGCA TCAAGTGACC AACAGGAAA AACCGCCCT TAACATGGCC CGCTTTATCA
 GTAGCCATAG TAATGGGGGT ACTTGCTCTTT AAGGGGAAT GTGCCTCCGT AGTTCACCTGG TTGTCTCTTT TTTCGGGGA ATTGTACCGG GCGAAATAGT

 301 GAAGCCAGAC ATTAACGCTT CTGAGAAAAC TCAACGAGCT GGACGGGAT GAACAGGAG ACATCTGTGA ATCGGTTAC GACCAGCTG ATGAGCTTTA
 CTTCCGTCTG TAATTGGGAA GACCTCTTTG AGTTGCTGA CCTGCGCTTA CTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTCCGAC TACTCGAAAT

 401 CCGCAGGATC CGGAAATGT AAACGTTAAT ATTTTGTAA AATTCGCGTT AAATTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA
 GCGCTCCTAG GCCTTTAACA TTGCAATTA TAAACAAT TTAAGCGCAA TTAAACAACA ATTTAGTGA GTAAAAAATT GGTATCCGG CTTTAGCCGT

 501 AAATCCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT GAGTGTTGTT CCAGTTTGA ACAAGAGTCC ACTATTAAG AACGTGGACT CCAACGTCAA
 TTTAGGGAAT ATTTAGTTTT CTATCTGGC TCTATCCAA CTCACACAA GGTCAAACCT TGTCTCAGG TGATAATTTC TTGCACCTGA GGTTCAGTT

 01 AGGGCGAAA ACCGTCTATC AGGGCTATGG CCCACTACGT GAACCATCAC CCTAATFCAAG TTTTITGGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC
 TCCCGCTTTT TGGCAGATAG TCCCGATACC GGTGATGCA CTTGGTAGTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTTCTGTA TTTAGCCTTG

 701 CCTAAAGGA GCGCGCGATT TAGAGCTTGA CCGGGAAGC CCGGAACGT GCGGAGAAG GAAGGAGAAG AAGCGAAAG AGCGGGCGCT AGGGCGCTGG
 GGATTTCCCT CCGGGGCTAA ATCTCGAAT ATCTCGAAT CCCCCTTTTC GCGCTTTGCA CCGCTCTTCT CTTCCCTTCT TTCCGCTTTC TCGCCCGGA TCCCGCGACC

 801 CAAGTGTAGC GGTACGCTG CCGGTAAACA CCACACCCG CCGCTTAAT GCGCGCTAC AGGGCGCTC CCGATCCTGC CTCGCGCGTT TCGGTGATGA
 GTTCACATCG CCAGTCGAC GCGCATTTGT GGTGTGGCG GCGGAATTA CCGGCGGATG TCCCGCGCAG GCCTAGGAGG GAGCGCGCAA AGCCACTACT

 901 CCGTGAAAAC CTCTGACACA TGCAGCTGCC GGAGACGCTC ACAGCTTGT TGTAAAGCGA TGCCGGGAGC AGACAAGCC GTACGGGCG GTACGGGCT
 GCCACTTTTG GAGACTGTGT ACGTCCAGG CCTCTGCCAG TGTCGAACAG ACATTCGCCT ACGGCGCTC TCTGTTCGG CAGTCCCGG CAGTCGCCCCA

 101 GTTGGCGGGT GTCGGGGCG AGCCATGACC CAGTCACGTA GCGATAGCG AGTGATATCT GGTAACTA TCGGGCATCA GAGCAGATTG TACTGAGAGT
 CAACCGCCCA CAGCCCCGG TCGGTACTGG GTCAGTGCAT CGCTATCGCC TCACATATGA CCGAATTGAT ACGCGTAGT CTCGTCTAAC ATGACTCTCA

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FIG. 25E

4101 GCACCATATG CGGTGTGAAA TACCGCACAG ATCGGTAAGG AGAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC
 CGTGGTATAC GCCACACTTT ATGGCGTGTG TACGCATTCC TCTTTTATGG CGTAGTCCGC GAGAGGCGA AGGAGCGAGT GACTGAGCGA CGCGAGCCAG

 4201 GTTCGGCTGC GCGGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT ATCCACAGAA TCAGGGGATA AGCAGGAAA GAACATGTGA GCAAAAGGCC
 CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCGGCC ATTATGCCAA TAGGTGTCTT AGTCCCTAT TCGTTCCTTT CTGTACACT CGTTTCCGG

 4301 AGCAAAAGGC CAGGAACCGT AAAAAGGCG CGTTGCTGGC GTTTTTCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG
 TCGTTTTCCG GTCCCTGGCA TTTTTCGGC GCAACGACCG CAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT TTAGCTCGA GTTCAGTCTC

 4401 GTGGCGAAC CCGACAGGAC TATAAGATA CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC TCGCGCTTAC CCGATACCTG
 CACCGCTTTG GGCTGTCTG ATATTCTAT GGTCCGCAA GGGGACCTT CGAGGAGCA CCGGAGGGA CAAGGCTGGG ACGGCGAATG GCCTATGGAC

 4501 TCCGCTTTC TCCCTTCGGG AAGCGTGGG CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGCTG AGTTCGCTG CTCCAAGCTG GGTGTGTGTC
 AGCGGGAAG AGGGAAGCCC TTCCGACCGC GAAAGATAT CGAGTCCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTTCGAC CCGACACACG

 4601 ACGAACCCC CGTTCAGCCC GACCGCTGG CTTTATCCG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC
 TGCTTGGGG GCAAGTCGGG CTGGCGACG GGAATAGGCC ATTGATAGCA GAATCAGGT TGGGCCATTG TGTGCTGAAT AGCGGTGACC GTCGTCTGGT

 4701 TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTCT TGAAGTGGT GCCTAACACTA GAAGGACAGT ATTTGGTATC
 ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA TGCTCAAGA ACTTCACCAC CGGATTGATG CCGATGTGAT CTTCCTGTCA TAAACCATAG

 4801 TGGGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG GTAGCTCTTG ATCCGGCAA CAAACACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC
 ACGCGAGAG ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC CATCGAGAAC TAGGCCGTTT GTTTGGTGGC GACCATCGCC ACCAAAAA CAAACGTTTCG

 4901 AGCAGATTAC GCGCAGAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGT CTGACGCTCA GTGGAACGAA AACTCAGCTT AAGGGATTTT
 TCGTCTAATG CCGCTCTTTT TTTCTTAGAG TTTCTTAGG AAATAGAAA AGATGCCCCA GACTGCGAGT CACTGTGCTT TTGAGTGCAA TTCCCTFAAAA

 5001 GGTCAATGAGA TTATCAAAA GGATCTTCAC CTAGATCTT TTAAATTAAT AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC
 CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCAGGAA AATTTAATTT TTACTTCAA ATTTAGTTAG ATTTCAATATA TACTCATTTG AACCAGACTG

5101 AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTAAT TCGTTTCATCC ATAGTTGCCT GACTCCCGCT CGCTAGATA ACTACGATAC
 TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG

 5201 GGGAGGGCTT ACCATCTGGC CCCAGTGTG CAATGATACC GCGAGACCCA CGCTCACCGG CTCAGATTT ATCAGCAATA AACAGACCAG CCGGAAGGGC
 CCTCCCGAA TGGTAGACCG GGGTCACGAC GTTACTATGG CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCGTTAT TTGGTCGGTC GGCCTTCCCG

 5301 CGAGCGCAGA AGTGGTCTCT CAACCTTATC CGCTCCCATC CAGTCATTA ATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGGCG
 GCTCGGTCT TCACCAGGAC GTTGAAATAG GCGGAGGTAG GTGAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA GCGGTCAATT ATCAAAACGG

 5401 AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCTGTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT
 TTGCAACAAC GGTAAAGCAG TCCGTAGCAC CACAGTCCGA GCAGCAAAAC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA

 5501 CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATCA CTCATGGTTA TGGCAGCACT
 GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG AGGCTAGCAA CAGTCTTCAT TCAACCGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA

 5601 GCATAATTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA TTCTGAGAAAT AGTGTATCG GCGACCGAGT
 CGTATTAAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA AGACACTGAC CACTCATGAG TTGTTTCACT AAGACTCTTA TCACATACGC CGCTGGCTCA

 5701 TGCTCTTGCC CCGCGTCAAC ACGGGATAAT ACCGGCCAC ATAGCAGAAC TTAAAAAGTG CTCATCATTG GAAAAAGTTC TTCGGGGCGA AAACCTCTCA
 ACGAGAACGG GCCGCAGTTG TGCCCTATTA TGGCGCGGTG TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTTGCAAG AAGCCCCGCT TTTGAGAGTT

 5801 GGATCTTACC GCTGTTGAGA TCCAGTTTGA TGTAAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC AGCGTTTCTG GGTGAGCAAA
 CCTAGAAATGG CGACAATCT AGGTCAAGCT ACATTTGGTG AGCAGGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAGAC CCACCTCGTTT

 5901 AACAGGAAGG CAAAATGCCG CAAAAAAGG AATAAGGGG ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG
 TTGTCCTTCC GTTTTACGGC GTTTTTTCCC TTATTTCCCG TGTGCTTTA CAACCTATGA GTATGAGAAG GAAAAAGTTA TAATAACTTC GTAATAATGC

 6001 GGTATTGTC TCATGAGCGG ATACATATTT GAATGATATT AGAAAAATAA ACAAAATAGG GTTCCGGCGA CATTTCCCG AAAAGTGCCA CCTGACGTCT
 CCAATAACAG AGTACTCGCC TATGTATAAA CTTACATAAA TCTTTTTTAT TTGTTATCCC CAAGGCGGT GTAAAGGGG TTTTTCACGGT GGACTGCAGA

101 AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG GCGTATCAG AGCCCTTTC GTCTTCAATA CAGGTAGACC TTTCGTAGAG ATGTACAGTG
 TTCTTTGGTA ATAATAGTAC TGTAATGGGA TATTTTATATC CGCATAGTGC TCCGGGAAG CAGAAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTAC

201 AAATCCCCGA AATTATACAC ATGACTGAAG GAAGGAGCT CGTCATTCCC TGCCGGGTTA CGTCACCTAA CATCACTGTT ACTTAAAAA AGTTTCCACT
 TTTAGGGGCT TTAATATG TGACTGACTTC CTTCCCTCGA GCAGTAAGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAATTTTTT TCAAAGGTGA

301 TGACACTTIG ATCCCTGATG GAAAACGCAT AATCTGGGAC AGTAGAAAG GCTTCATCAT ATCAAAATGCA AGTACAAAG AAATAGGGCT TCTGACCTGT
 ACTGTGAAAC TAGGGACTAC CTTTITGGTA TTAGACCCCTG TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGCATGTTTC TTATATCCCGA AGACTGGACA

101 GAAGCAACAG TCAATGGGCA TTGTATTAAG ACAAACCTATC TCACACATCG ACAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT
 CTTCGTGTGC AGTTACCCGT AAACATATTC TGTTGATAG AGTGTGTAGC TGTTTGGTTA TGTTATGTCC ATCTGGAAG CATCTCTACA TGTCACTTTA

101 CCCCAGAAAT ATACACATGA CTGAAGGAAG GGAGCTCGTC ATTCCCTGCC GGGTTACGTC ACCTAACATC ACTGTTACTT TAAAAAAGTT TCCACTTGAC
 GGGGCTTTAA TATGTGTACT GACTTCTTTC CCTCGAGCAG TAAGGAGCGG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTITCAA AGGTGAACTG

01 ACTTTGATCC CTGATGGAAA ACGCATATC TGGGACAGTA GAAAGGCTT CATCATATCA AATGCAACGT ACAAGAAAT AGGGCTCTG ACCGTGGAAG
 TGAACACTAGG GACTACCTTT TCGGTATTAG ACCGTGTCAT CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTITCTTTA TCCCCAAGAC TGGACACTTC

101 CAACAGTCAA TGGGCATTG TATAAGACAA ACTATCTCAC ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTTCGT AGAGATGTAC AGTGAATCC
 GTTGTAGTT ACCCGTAAAC ATATTCTGTT TGATAGAGTG TGTAGCTGTT TGTTTATGTT AGATGTCCAT CTGGAAGCA TCTCTACATG TCACTTTAGG

101 CCGAAATTAT ACACATGACT GAAGGAAGG AGCTCGTCAT TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTACTTTA AAAAAGTTTC CACTTGACAC
 GGCCTTAATA TGTGTACTGA CTTCTTCCC TCGAGCAGTA AGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACCTGTG

101 TTTGATCCCT GATGAAAAC GCATAATCTG GGACAGTAGA AAGGCTTCA TCAATACAAA TGCAACGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA
 AAAC TAGGGA CTACCTTTTG CGTATTAGAC CTTGTCTATCT TTCCCCAAGT AGTATAGTTT ACGTTGCATG TTTCTTTATC CCGAAGACTG GACACTTCGT

101 ACAGTCAATG GGCATTGTGA TAAGACAAAC TATCTCACAC ATCGACAAAC CAATACAATC
 TGTCACTTAC CCGTAAACAT ATTCTGTTTG ATAGAGTGTG TAGCTGTTTG GTTATGTTAG

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FIG. 25 H

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1 GAATTCAACT TCTCCATACT TTGGATAAGG AATAACAGAC ATGAAAATATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTATAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACCTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTACGA AGCGTTATAC CGGTTTATAC TGGTTGTGCG CAACTAACTA GTCCATCTCC

201 GGGCGTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
CCGCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAGG CGCTAATGCA TTCTTTCAAT AACTTCGTAG GACGAGTCAT

301 AAAAGTTAAT CTTTTCACAA GCTGTCAATA AGTTGTCACG GCCGAGACTT ATAGTCGGTT TGTTTTTTAT TTTTAATGTA TTTGTAACTA GTACGCAAGT
TTTTCAAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAA AGGGTATGTA GAGTTGAGG TGATTTTATG AAAAGAATA TCGCAATTCT TCTTGCATCT ATGTTCTGTT TTTCTATTGC TACAAATGCC
AGTGCATTTT TCCCATATCAT CTCCAACCTC ACTAAATATC TTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG
1 M K K N I A F L L A S M F V F S I A T N A
^start of stII sequence

501 TATGCATCG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TCPCGCCCTC TGTGGCGCAT AGGTCACCA TCACCTGCGG TGCCAGTCAG GATGTGTCCA
ATACGTAGGC TATAGGTCTA CTGGGTCAGG GGCTCGAGG ACAGGCGGAG ACACCGCTA TCCCACTGTT AGTGGACGGC ACGGTCAGTC CTACACAGGT
22 Y A S D I Q M T Q S P S L S A S V G D R V T I T C R A S Q D V S T
^light chain start

601 CTGCTGTAGC CTGCTATCAA CAGAAACCAG GAAAGCTCC GAAGCTTCTG ATTTACTCGG CATCTTCTCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG
GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG CTTTGAAGAC TAAATGAGCC GTAGGAAGGA GATGACCT CAGGGAAGAG CGAAGAGACC
56 A V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G
^CDR-L2

701 TAGCGGTTCC GGGACGGATT TCACCTCGAC CATCAGCAGT CTGCAGCGG AAGACTTCG AACTTATATC TGTACGCAAT CTTTACTAC TCCTCCACAG
ATCGCCAAGG CCTGCTCTAA AGTGAGACTG GTAGTCGTCA GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTA GAATATGATG AGGAGGTTGC
89 S G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T
^CDR-L3

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FIG. 26A

1 TTCCGACAGG GTACCAAGGT GGAGATCAAA CGAACTGTGG CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAATCT GGAAGTGCCT
 AAGCTGTCC CATGGTTCCA CCTCTAGTTT GCTTGACACC GACGTGGTAG ACAGAAGTAG AAGGGCGGA GACTACTCGT CAACCTTAGA CCTTGACGGA
 2 F G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S
 1 CTGTTGTGTG CCTGTGTAAT AACTTCTATC CCAGAGAGGC CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC
 GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG GTTTCATGTC ACCTTCACC TATTGCGGA GGTAGCCCA TTGAGGGTCC TCTCAGATG
 6 V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T
 1 AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC ACCCTGACGC TGAGCAAGC AGACTACGAG AAACACAAAG TCTACGCCCTG CGAAGTCACC
 TCTCGTCCCTG TCGTTCCTGT CGTGGATGTC GGAGTCGTG TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG
 9 E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T
 1 CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAGGACC
 GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCGAAGTTGT CCCCTCTCAC ACCACGGTGG AGGCCATACC GACTAGGCTT GGCAAGGGC CCATTCCCTGG
 2 H Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L
 ^end of light chain, start of gD tag
 1 TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG TGGCCCTAGT AGCAAGTTC ACCTAAAG GGTGAGGTG ATTTTATGAA
 ACCGTATTGA GCTCCGACTA GGAGATCGGG CCTGCGTAGC ACCGGGATCA TCGGTTCAAG TGCATTTTTC CCATGATCT CCAACTCCAC TAAATACTT
 6 A O
 3
 M K
 ^start of stII
 1 AAAGAAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGGTA CGCTGAGGT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG
 TTTCTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTGGCAT GCGACTCAA GTCGACCACC TCAGACCGCC ACCGGACCAC
 1 K N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G L V
 ^start of heavy chain
 1 CAGCCAGGGG GCTCACTCCG TTTGTCTCTGT GCAGTCTCTG GCTTCAACAT TAAAGACACC TATATACACT GGGTCCGTCA GGGCCCGGT AAGGCCTGG
 GTCGTCCTCC CGAGTGAGGC AAACAGGACA CGTCAAGAC CGAAGTTGTA ATTTCTGTGG ATATATGTA CCCACGAGT CCGGGGCCCA TTCCCGGACC
 3 Q P G G S L R L S C A A S G F N I K D T Y I H W V R Q A P G K G L E
 ^CDR-H1

FIG. 26b

1501 AATGGGTTGC AAGGATTAT CCTACGAATG GTTATACATAG ATATGGCGAT AGCGTCAAGG GCGTTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC
 TTACCCAACG TTCCCTAAATA GGATGCTTAC CAATATGATC TATACGGCTA TCGCAGTTCC CGGCAAAGTG ATATTCCGGT CTGTGTAGGT TTTTGTGTGG
 47 W V A R I Y P T N G Y T R Y A D S V K G R F T I S A D T S K N T A
 ^CDR-H2
 1601 CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC GTCTATTATT GTAGCCGGTG GGGAGGGGAC GGCTTCTATG CTATGGACTA CTGGGGTCAA
 GATGGATGTT TACTTGTGGA ATTCTCGACT CCTGTGACGG CAGATAATAA CATCGGGGAC CCCTCCCTCG CCGAAGATAC GATACCTGAT GACCCCAAGTT
 80 Y L Q M N S L R A E D T A V Y Y C S R W G G D G F Y A M D Y W G Q
 ^CDR-H3
 1701 GGAACACTAG TCACCGTCTC CTCGGCCCTC ACCAAGGGCC CATCGGTCTT CCCCTGGCA CCTCTCTCCA AGAGCACCTC TGGGGGCACA GCGGCCCTGG
 CCTTGTGATC AGTGGCAGAG GAGCCGGAGG TGGTTCCCGG GTAGCCAGAA GGGGACCGT GGGAGGAGGT TCTCTGGAG ACCCCCGTGT CGCCGGGACC
 113 G T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G
 1801 GCTGCCTGGT CAAGGACTAC TTCCCCGAA CCGTGACGGT GTCGTGAAC TCAGGGGCCC TGACACAGCG CGTGACACACC TTCCCGGGCTG TCCTACAGTC
 CGACGGACCA GTTCTGTATG AAGGGGCTTG GCCACTGCCA CAGCACCTTG AGTCCGCGGG ACTGCTGCGC GCACGTGTGG AAGGGCCGAC AGGATGTGAC
 147 C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S
 1901 CTCAGGACTC TACTCCCTCA GCAGCGTGGT GACCGTGCCC TCCAGCAGCT TGGGCACCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC
 GAGTCCTGAG ATGAGGGAGT CGTGCACACA CTGGCACGGG AGGTGCTCGA ACCCGTGGGT CTGGATGTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTGG
 180 S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T
 2001 AAGGTCGACA AGAAAGTTGA GCCCAATCT TGTGACAAA CTCACGGCGG CATGAACAG CTAGAGGACA AGGTCAAGA GCTACTCTCC AAGAATACC
 TTCCAGCTGT TCTTTCACT CGGGTTTAGA ACACGTGTTT GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTTGATGG
 213 K V D K K V E P K S C D K T H G R M K Q L E D K V E E L L S K N Y H
 ^end of heavy chain, start of leucine zipper
 2101 ACCTAGAGAA TGAAGTGGCA AGACTCAAAA AACTTGTGCG GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGCTTCCGGT GATTGTGATT ATGAAGAAGAT
 TGGATCTCTT ACTTCACCGT TCTGAGTTT TTGAACAGCC CCTCGCGCCT TTGCAATCAC CGCCACCGAG ACCAAGGCCA CTAATACTAA TACTTTTCTA
 247 L E N E V A R L K K L V G E R G K L S G G S G S G D F D Y E K M
 end of leucine zipper, start of gene III coat protein (267-end)^

FIG. 26C

2201 GGCAACCGCT AATAAGGGG CTATGACCGA AAATGCCGAT GAAAACGGC TACAGTCTGA CGCTAAAGGC AAATTGATT CTGTGCGTAC TGATTACGGT
 CCGTTTGGCA TTATTCCCC GATACCTGGT TTTACGGCTA CTTTTCGGC ATGTCAGACT GCGATTCCG TTTGAATAA GACAGCGATG ACTAATGCCA
 280 A N A N K G A M T E N A D E N A L Q S D A K G K L D S V A T D Y G
 2301 GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCCTG CTAATGGTAA TGGTGCTACT GGTGATTTTG CTGGCTCTAA TTCCCAAAATG GCTCAAGTCG
 CGACGATAGC TACCAAAAGTA ACCACTGCAA AGCCCGGAAC GATTACCAAT ACCACGATGA CCACATAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC
 313 A A I D G F I G D V S G L A N G N G A T G D F A G S N S Q M A Q V G
 2401 GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTACCT TCCCTCCCTC AATCGGTGA ATGTCGCCCT TTTGTCTTTA GCGCTGGTAA
 CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT TATAATGGA AGGAGGGAG TTAGCCAACT TACAGCGGGA AAACAGAAAT CCGGACCAAT
 347 D G D N S P L M N N F R Q Y L P S L P Q S V E C R P F V F S A G K
 2501 ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTTCGTT TCTTTTATAT GTTGCCACCT TTATGTTATG ATTTTCTACG
 TGGTATACCT AAAAGATAAC TAACACTGTT TTATTTGAAT AAGGCACCAC AGAAACGCAA AGAAATATA CAACGGTGA AATACATACA TAAAAGATGC
 380 P Y E F S I D C D K I N L F R G V F A F L L Y V A T F M Y V F S T
 2601 TTTGCTAACA TACTGCGTAA TAAGGACTCT TAATCATGCC AGTTCTTTTG GCTAGCGCGG CCTATACCT TGCTGCGCTC CCGCGCTGTC GTCGCGGTGC
 AAACGATTGT ATGACGCATT ATTCTCTAGA ATTAGTACGG TCAAGAAAC CGATCGCGG GGAATATGA ACAGACGGAG GGGCGCAACG CAGCGCCACG
 413 F A N I L R N K E S O
 2701 ATGGAGCCGG GCCACCTCGA CCTGATGGA AGCCGGCGGC ACCTCGCTAA CCGATTACCC ACTCCAAGAA TTGGAGCCAA TCAATTCTTG CGGAGAATCG
 TACCTCGGCC CCGTGGAGCT GGACTTACCT TCGGCCGCGC TGGAGCGATT GCTAAGTGG TGAGGTTCTT AACCTCGGTT AGTTAAGAAC GCCTCTTGAC
 2801 TGAATGCGCA AACCAACCCT TGGCAGAACA TATCCATCGC GTCCGCCATC TCCAGCAGCC GCACGCGGG CATCTCGGGC AGCGTTGGGT CCTGGGCCACG
 ACTTACGCGT TTGGTTGGGA ACCGTCTTGT ATAGGTAGCG CAGCGGTAG AGGTGCTGG CGTGCGCGC GTAGAGCCG TCGCAACCCA GGACCGGTGC
 2901 GGTGCGCATG ATCGTGCTCC TGTCGTTGAG GACCCGGGTA GGCTGGCGG GTTGCCCTTAC TGCTTAGCAG AATGAATCAC CGATACCGA CGGAACGTGA
 CCACGCGTAC TAGCAGGAG ACAGCAACTC CTGGGCCGAT CCGACCGCCC CAACGGAATG ACCAATCGTC TTACTTAGTG GCTATGCGCT CGCTTGCACT
 3001 AGCGACTGCT GCTGCAAAAC GTCGCGACC TGAGCAACAA CATGAATGGT CTTGCGTTTC CCGTTTTCGT AAAGTCTGGA AACCGGGAAG TCAGCGCCCT
 TCGCTGACGA CGACGTTTTC CAGACGCTTG ACTCGTTTGT GTACTTACCA GAAGCCAAAG GCACAAAGCA TTTTCAGACCT TTGCGGCTTC AGTCGCGGGA

FIG. 26D

3101 GCACCAATTAT GTTCCGGATC TGCATCCGAG GATGCTGCTG GCTACCCCTGT GGAACACCTA CATCTGTATT AACGAAGCGC TGGCATGAC CCTGAGTGAT
 CGTGGTAATA CAAGGCCCTAG ACGTAGGCTC CTACGACGAC CGATGGACA CTTGTGGAT GTAGACATAA TTGCTTCGCG ACCGTAACTG GGACTCACTA
 3201 TTTTCTCTCG TCCCGCCGCA TCCATACCGC CAGTTGTTTA CCTCACAAC GTTCCAGTAA CCGGSCATGT TCATCATCAG TAACCCGTAT CGTGAGCATC
 AAAAGAGACC AGGCGGCGT AGGTATGGC GTCAACAAT GGGAGTGTG CAAGTCAIT GGCCTGTACA AGTAGTAGTC ATTGGGCATA GCACTCGTAG
 3301 CTCTCTCTCT TCAATCCGAT CATACCCCC ATGAACAGAA ATTCCCCCTT ACACGGAGC ATCAAGTGAC CAACAGGAA AAAACCCGCC TTAACATGGC
 GAGAGAGCAA AGTAGCCATA GTAATGGGG TACTTGTCTT TAAGGGGAA TGTCCCTCCG TAGTTCACGT GTTGTCTCTT TTTTGGCGGG AATTGTACCG
 3401 CCGCTTTATC AGAAGCCAGA CATTAACGCT TCTGGAGAAA CTCAACGAGC TGGACGCGGA TGAACAGGCA GACATCTGTG AATCGCTTCA CGACCACGCT
 GCGCAATAG TCTTCGGTCT GTAATTGCGA AGACCTCTTT GAGTTGCTCG ACCTGGCCTT ACTTGTCCGT CTGTAGACAC TTAGCGAAGT GCTGTGCGA
 3501 GATGAGCTTT ACCGCAGGAT CCGGAAATG TAAACGTTAA TATTTTCTTA AAATTCGCGT TAAATTTTG TTAATCAGC TCATTTTITA ACCAATAGGC
 CTAATCGAAA TGGCGTCTTA GGCCTTTAAC ATTTGCAATT ATAAACAAT TTAAAGCGCA ATTTAAGTCG AGTAAAAAT TGGTTATCCG
 3601 CGAAATCGC AAAATCCCTT ATAAATCAA AGAATAGACC GAGATAGGT TGAGTGTGT TCCAGTTTGG AACAAAGATC CACTATTAAA GAACCTGGAC
 GCTTAGCCG TTTTAGGGAA TATTTAGTTT TCTTATCTGG CTCTATCCCA ACTCACAACA AGTCAAAACC TTGTTCTCAG GTGATAATTT CTGACACCTG
 3701 TCCAAAGTCA AAGGGGAAA AACCGTCTAT CAGGGCTATG GCCCACTAG TGAACCATCA CCTAATCAA GTTTTITGG GTGAGGTGC CGTAAAGCAC
 AGGTGTCAGT TTCCCGCTTT TTGGCAGATA GTCCCGATAC CGGTGATGC ACTTGTAGT GGGATTAGT CAAAAAACCC CAGCTCCACG GCATTTCTGT
 3801 TAAATCGGA CCTAAAGGG AGCCCCCGAT TTAGAGCTTG ACGGGGAAAG CCGGCGAAG TGGCGAGAAA GGAAGGGAAG AAAGCGAAG GAGCGGGCGC
 ATTTAGCCTT GGGATTCCC TCGGGGGCTA AATCTCGAAC TGCCCCCTTC GCGCGTTC ACCGCTCTTT CCTTCCCTTC TTTCCCTTC CTGCGCCGCG
 3901 TAGGGCGCTG GCAAGTGTAG CCGTCACGCT GCGCGTAACC ACCACACCG CCGCGCTTAA TGGCGCGCTA CAGGGCGCTT CCGGATCCTG CCTCGCGCT
 ATCCCGCGAC CATTACATC GCCAGTGGA CCGGCAITGG TGGTGTGGG GCGCGGAATT ACGCGCGAT GTCCCGCGCA GGCCTAGGAC GGAGCGCGCA
 4001 TTCCGCTGAT ACGGTGAAA CCTCTGACAC ATGACGCTCC CCGAGACGCT CAGAGACGCT CTGTAAGCGG ATGCCGGGAG CAGACAAGCC CGTCAGGGC
 AAGCCACTAC TGCCACTTTT GGAGACTGTG TAGGTGAGG GCCTCTGCCA GTGTGGAACA GACATTCGCC TACGGCCCTC GTCTGTTCGG GCAGTCCCGC
 4101 CGTCAGCGG TGTGGCGGG TGTGCGGGG CAGCCATGAC CCAGTCACGT ACCGATAGCG GAGTGTATAC TGGTTAACT ATCGGCGATC AGAGCAGATT
 GCAGTCGCC ACAACGGCC ACAGCCCCG GTCCGTACTG GTTCAGTGCA TCGCTATCG CTCACATATG ACCGAATGA TACGCCGTAG TCTCGTCTAA

FIG. 24E

4201 GTACTGAGAG TGCACCATAT GCGGTGTGAA ATACCGCACA GATCGGTAAG GAGAAAATAC CGCATCAGGC GCTCTTCGGC TTCTCTCGCTC ACTGACTCGC
 CATGACTCTC ACGTGGTATA CGCCACACTT TATGGCGTGT CTACGCATTC CTCCTTTATG GCGTAGTCCG CGAGAAGGG AAGGAGCGAG TGACTGAGCG

 4301 TCGGCTCGGT CGTTGCGGTG CCGCGAGCGG TATCAGCTCA CTCAAAGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG
 ACGGAGCCCA GCAAGCCGAC GCGGCTCGCC ATAGTCGAGT GAGTTTCCGC CATATGCCA ATAGGTCT TAGTCCCTA TTGCGTCTT TCTTGTACAC

 4401 AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAGGCC GCGTTGCTGG CGTTTTCCTA TAGGTCCTCG CCCCCTGACG AGCATCAAA AAATCGACGC
 TCGTTTTCGG GTCGTTTTCG GGTCTTTTCC GGTCTTTCCG ATTTTTCGG CGCAACGACC GCAAAAAGGT ATCCGAGGCG GGGGACTGC TCGTAGTCTT TTTAGCTGCG

 4501 TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGTCCCTCG TCGGCTCTCC TGTTCCGACC CTGCCGCTTA
 AGTTCAGTCT CCACCGCTTT GGGCTGTCTT GATATTTCTA TGGTCCGCAA AGGGGACCT TCGAGGGAGC ACGGAGAGG ACAAGGCTGG GACGGCGAAT

 4601 CCGGATACCT GTCCGCCCTTT CTCCCTTCGG GAAGCGTGGC GCTTCTCTAT AGCTCAGCT GTAGGTATCT CAGTTCGGTG TAGTTCGTTT GCTCCAAAGCT
 GGCCATATGA CAGGCGGAAA GAGGGAAGCC CTTCGACCG CGAAGAGTA TCGAGTCCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA

 4701 GGGCTGTGTG CACGAACCCC CGCTTCAGCC CGACCGGTGC GCCTTATCCG GTAACATATCG TCTTGAGTCC AACCCGGTAA GACAGGACTT ATCGCCACTG
 CCCGACACAC GTGCTTGGG GGCAGTCCG GCTGGCGACG CGGAATAGC CATGTATAGC AGAATCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC

 4801 GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGTG GGCCTAACHA CGGCTACACT AGAAGGACAG
 CGTCGTCCGT GACCATTTGC CTAATCGTCT CGTCCATATC ATCCGCCAG ATGTCTCAAG AACTTCACCA CCGGATTGAT GCGGATGTA TCTTCTCTGTC

 4901 TATTTGGTAT CTGGGCTCTG CTGAAGCCAG TTACTTTCGG AAAAAGAGTT GGTAGTCTTT GATCCGGCAA ACAAAACCACC GCTGGTAGCG GTGGTTTTTT
 ATAAACCAT GACGCGAGAC GACTTCGGTC AATGGAAGCC TTTTCTCTCA CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA

 5001 TGTTTGCAAG CAGCAGATTA CCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGG TCTGACGCTC AGTGAACGA AAATCAGCT
 ACAACGTTT GTCGTCTAAT GCGGCTCTTT TTTTCTCTAGA GTTCTTCTAG GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGCT TTTGAGTGCA

 5101 TAAGGGATTT TGGTCATGAG ATTATCAAAA AGGATCTTCA CCTAGATCTT TTTAAATTA AAATGAAGTT TTAAATCAAT CTAAAGTATA TATGAGTAAA
 ATTCCCTAAA ACCAGTACT TAATAGTTTT TCCTAGAAGT GGATCTAGGA AAATTTAATT TTTACTTCAA AATTAGTTA GATTTCATAT ATACTCATTT

 5201 CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG ATCTCTCTAT TTCTGTCATC CATAGTTGCC TGACTCCCCG TCGTGTAGAT
 GAACCAAGCT GTCAATGGTT ACGAATTAGT CACTCCGTGG ATAGAGTCG TAGACAGATA AAGCAAGTAG GTATCAACGG ACTGAGGGG AGCACATCTA

FIG. 26f

5301 AACTACGATA CGGAGGGCT TACCATCTGG CCCAGTGTCT GCAATGATAC CGCAGAGACC AGCTCACCG GCTCCAGATT TATCAGCAAT AAACAGCCA
 TTGATGCTAT GCCCTCCGA ATGGTAGACC GGGGTACGA CGTTACTATG GCGCTCTGG TCGAGTGGC CGAGTCTAA ATAGTCGTTA TTTGGTGGT

 5401 GCCGGAAGG CCGAGCGCAG AAGTGGTCTT GCAACTTTAT CCGCCTCCAT CCAGTCTATT AATGTTGCC GGAAGCTAG AGTAAGTAGT TCGCCAGTTA
 CGGCCTTCCC GGCTCGGCTC TTCACCAGGA CGTTGAAATA GCGGAGGTA GGTCAATAA TTAACAACGG CCCTTCGATC TCATTTCATCA AGCGTCAAT

 5501 ATAGTTGGG CAACGTTGTT GCCATGTCTG CAGGATCTGT GGTGTACCG TCGTCTGTTG GTATGGCTTC ATTCAGCTCC GGTCCCAAC GATCAAGGCG
 TATCAAAAGC GTTGCAACAA CCGTAACGAC GTCCGTAGCA CCACAGTGG AGCAGCAAC CATACCGAAG TAAGTCGAGG CCAAGGGTTG CTAGTTCGCG

 5601 AGTTACATGA TCCCCCATGT TGTGCAAAA TCGTCTGCTC AGGGTTAGC TCCTTCGGTC CTCGATCTGT TGTCAAGAAGT AAGTTGGCG CAGTGTATC ACTCATGGTT
 TCAATGTACT AGGGGGTACA ACACGTTTTT TCGCCAATCG AGGAAGCCAG GAGGCTAGCA ACAGTCTTCA TTCAACCGGC GTCACAATAG TGAGTACCAA

 5701 ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA TAGTGTATGC
 TACCCTCGTG ACGTATTAAG AGAATGACAG TACGGTAGGC ATTCTACGAA ATCTTACGAA AAGACACTGA CCACTCATGA GTTGGTTCAG TAAGACTCTT ATCACAATAG

 5801 GCGACCGGAG TTGCTCTTGC CCGCGCTCAA CCGGGGATAA TACCGGCGCA CATAGCAGAA CTTTAAAGT GCTCATCATT GGAAAACGTT CTTCGGGGCG
 CCGTGGCTC AACGAGAACG GGCCGCGATT GTGCCCTATT ATGGCGCGGT GTATCGTCTT GAAATTTTCA CGAGTAGTAA CCTTTTGCAA GAAGCCCCG

 5901 AAAACTCTCA AGGATCTTAC CGCTGTTGAG ATCCAGTTCC ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTTAC CAGCGTTTCT
 TTTTGAGAGT TCCTAGATG CCGACAATC TAGGTCAAGC TACATGGGT TACATGGGT GAGCACTGAG AGTCGTAGAA AATGAAAAGT GTCGCAAGA

 6001 GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAGG GAATAAGGC GACACGGAAA TGTGATATAC TCATCTCTCT CCTTTTTCAT TATTATTGAA
 CCCACTCGTT TTTGTCTTTC CGTTTTCAGG CGTTTTCAGG CGTTTTCAGG CGTTTTCAGG CGTTTTCAGG CGTTTTCAGG CGTTTTCAGG CGTTTTCAGG CGTTTTCAGG

 6101 GCATTTATCA GGGTTATGTT CTCATGAGCG GATACATATT TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCGGCG ACATTTTCCC GAAAAGTGCC
 CGTAAATAGT CCCAATAACA GAGTACTCCG CTATGTATAA ACTTACATAA ATCTTTTAT TTGTTTATCC CCAAGGGCGG TGTAAGGGG CTTTTTCACGG

 6201 ACCTGACGTC TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAATA GGCATATCAC GAGGCGCTTT CGTCTTCAAT ACAGGTAGAC CTTTCGTAGA
 TGGACTGCAG ATTCTTTGGT AATAATAGTA CTGTAATGG ATATTTTAT CCGCATAGTG CTCGGGAAA GCAGAAATTA TGTCCATCTG GAAAGCATCT

 6301 GATGTACAGT GAAATCCCCG AAATATATCA CATGACTGAA GGAAGGGAGC TCGTCATTC CCGCGGGT ACGTCACCTA ACATCACTGT TACTTTAAAA
 CTACATGTCA CTTTAGGGG TTTAATATGT GTACTGACTT CCTTCCCTCG AGCAGTAAG GACGCGCAA TGCAGTGGAT TGTAGTGACA ATGAAATTTT

FIG. 26

6401 AAGTTTCCAC TTGACACTTT GATCCCTGAT GGAAAACGCA TAATCTGGGA CAGTAGAAG GGTTCATCA TATCAAAATGC AACGTACAAA GAAATAGGGC
 TTCAAAGGTG AACTGTGAAA CTAGGGACTA CCTTTTGGGT ATTAGACCCT GTCATCTTTC CCGAAGTAGT ATAGTTTACG TTGCATGTTT CTTTATATCCCG

 6501 TTCTGACCTG TGAAGCAACA GTCAATGGGC ATTGTATAA GACAAACTAT CTCACACATC GACAAACCAA TACAATACAG GTAGACCTTT CGTAGAGATG
 AAGACTGGAC ACTTCGTGT CAGTTACCCG TAAACATATT CTGTTTGATA GAGTGTGTAG CTGTTTGGGT ATGTTATGTC CATCTGGAAA GCATCTCTAC

 6601 TACAGTGAAA TCCCCGAAAT TATACACATG ACTGAAGGAA GGGAGCTCGT CATTCCTGTC CGGGTTACGT CACCTAACAT CACTGTTACT TTAATAAAGT
 ATGTCACCTT AGGGGCTTTA ATATGTGTAC TGACTTCCTT CCTCGAGCA GTAAGGAGC GCCCAATGCA GTGGATTGTA GTGACAAATGA AATTTTTC

 6701 TTCCACTTGA CACTTTGATC CCTGATGGAA AACGCATAAT CTGGACAGT AGAAGGGCT TCATCATATC AAATGCAACG TACAAAGAAA TAGGGCTTCT
 AAGGTGAAC GTGAAACTAG GGAATACCTT TTGCGTATTA GACCTGTCA TCCTTCCCGA AGTAGATAG TTTACGTTGC ATGTTTCTTT ATCCCGAAGA

 6801 GACCTGTGAA GCAACAGTCA ATGGGCAATTT GTATAAGACA AACTATCTCA CACATCGACA AACCAATACA ATCTACAGGT AGACCTTTCG TAGAGATGTA
 CTGGACACTT CGTTGTGAGT TACCCGTAAA CATATTCTGT TTGATAGAGT GTGTAGCTGT TTGTTTATGT TAGATGTCCA TCTGGAAAGC ATCTCTACAT

 6901 CAGTGAAATC CCCGAAATTA TACACATGAC TGAAGGAAGG GAGCTCGTCA TTCCCTGCCG GGTACGTCA CCTAACATCA CTGTTACTTT AAAAAAGTTT
 GTCACTTTAG GGGCTTTAAT ATGTGTACTG ACTTCCCTCC CTCGAGCAGT AAGGACGGC CCAATGCAGT GGATTGTAGT GACAATGAAA TTTTTCATAA

 7001 CCACTTGACA CTTTGATCCC TGATGGAAAA CGCATAATCT GGGACAGTAG AAAGGGCTTC ATCATATCAA ATGCAACGTA CAAAGAAATA GGGCTTCTGA
 GGTGAACGTG GAAACTAGG ACTACCTTTT GCGTATTAGA CCTGTCTATC TTTCCCGAAG TAGTATAGTT TACGTTGCAT GTTTCCTTAT CCCGAAGACT

 7101 CCTGTGAAGC AACAGTCAAT GGGCATTTGT ATAAGACAAA CTATCTACA CATCGACAAA CCAATACAAT C
 GGACACTTCG TTGTCAGTTA CCCGTAAACA TATTCTGTTT GATAGAGTGT GTAGCTGTTT GGTATGTGA G

FIG. 24 H

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1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTG TTTTCTTAT TGCTACAAAT GCCTATGAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CCGATACGTC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG
1 M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
^met
^start of stII signal sequence
^start of light chain

101 TGTCCGCCCTC TGTGGCGGAT AGGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC CTGGTATCAA CAGAAACCCAG GAAAAGCTCC
ACAGGCGGAG ACACCGGCTA TCCCAGTGGT AGTGGACGGC ACGGTACGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
^CDR-L1

201 GAAGCTTCTG ATTACTCGG CATCCTTTCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGCGGTTC GGGACGGATT TCACCTCTGAC CATCAGCAGT
CTTCGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCAAGG CCTGCGCTAA AGTGAGACTG GTAGTCGTCA
68 K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
^CDR-L2

301 CTGCAGCCGG AAGACTTCGC AACTTATTAC TGTACGCAAC ATTATACTAC TCCTCCACG TTTCGGACAGG GTACCAAGGT GGAGATCAA CGAACTGTGG
GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCGTTG TAATATGATG AGGAGGGTGC AAGCCTGTCC CATGTTGCCA CCTCTAGTTT GCTTGACACC
101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
^CDR-L3

401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAATCT GGAATGCCT CTGTTGTGTG CCTGCTGAAT AACITCTATC CCAGAGAGGC
GACGTGGTAG ACAGAAGTAG AAGGGCGGTA GACTACTCGT CAACTTTAGA CTTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A

501 CAAAGTACAG TGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG AGAGTGTAC AGACCAAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
GTTTCATGTC ACCTTCACAC TATTGCGGGA GGTAGGCCA TTGAGGGTCC TCTCACAGTG TCTGCTCTCTG TCGTTCTCTG CGTGGATGTC GGAGTCGTCG
168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S

601 ACCCTGACG TGAGCAAAGC AGACTACGAG AAACACAAG TCTACGCCCT GGAAGTCACC CATCAGGGCC TGAGTCGCC CGTCACAAAG AGCTTCAACA
TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGGGAC GCTTCAGTGG GTAGTCCCGG ACTCAGCGG GCAGTGTTC TCGAAGTTGT
201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

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FIG. 27A

701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAAGGACC TGGCATAACT CGAGGCTGAT CCTCTACGCC GGACGCATCG
 CCCCTCTCAC ACCACGGTGG AGGCCATACC GACTAGGCTT GGCAAAGGCG CCATTCCTGG ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC
 235 G E C G A S S G M A D P N R F R G K D L A O
 ^end of light chain, start of gd tag

 801 TGGCCCTAGT ACACAAGTTC ACCTAAAAAG GGTAACTAGA GGTGAGGTG ATTTTATGAA AAAGAATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT
 ACCGGGATCA TGGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAATACTTT TTTCCTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA
 -23 M K K N I A F L L A S M F V F
 ^start of stII

 901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCCTGGTG CAGCCAGGGG GCTCACTCCG TTTGTCTCTGT GCAGCTTCTG
 AGATAACGAT GTTTGGCGAT GCGACTCCAA GTCGACCCACC TCAGACCCGC ACCGGTCCCG CGAGTGAGGC AAACAGGACA CGTCGAAGAC
 -8 S I A T N A Y A E V Q L V E S G G G L V Q P G G S L R L S C A A S G
 ^start of heavy chain
 ^CDR-H1

 001 GCTTACCAT TAGTGGTCTT TGGATACACT GGGTGCGTCA GGGCCCGGCT AAGGGCCTGG AATGGGTTGC TTGGATTGCT CCTTATAGCG GCGCTACTGA
 CGAAGTGCTA ATCACCAGA ACCTATGTGA CCCACGCGAT CCGGGGCCCC TTCCCGGACC TTACCCCAACG AACCTAACGA GGAATATCGC CGCGATGACT
 27 F T I S G S W I H W V R Q A P G K G L E W V A W I A P Y S G A T D
 ^CDR-H2

 101 CTATGCCGAT AGCGTCAAGG GCGGTTTCAC TATAAGGCA GACACATCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
 GATACGGCTA TCGCAGTTC CCGCAAAGTG ATATTGCGGT CTGTGCTAGT TTTTGTGTGG GATGGATGTT TACTTGTCTGA ATTCTCGACT CCTGTGACGG
 60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

 201 GTCTATTATT GTGCAAGAGA GGGGGGCTTG TACTGGGTGT TCGACTACTG GGTCAAGGA ACACCTAGTCA CCGTCTCTCT GGCCTCCACC AAGGGCCAT
 CAGATAATAA CACGTTCTCT CCCCCCGAAC ATGACCCACA AGCTGATGAC CCCAGTTTCT TGTGATCAGT GGCAGAGGAG CCGGAGGTGG TTCCCGGGTA
 93 V Y Y C A R E G G L Y W V F D Y W G Q G T L V T V S S A S T K G P S
 ^CDR-H3

 301 CGGTCTTTCC CCTGGCACC TCCTCCAAGA GCACCTCTGG GGGCACAGCG GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGGTGC
 GCCAGAAGGG GGACCGTGG AGGAGGTCTT CGTGGAGACC CCGGTGTCG CCGGACCCGA CGGACCAAGT CCTGATGAG GGGCTTGGCC ACTGCCACAG
 127 V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S

FIG. 27B

1401 GTGGAACCTCA GCGGCCCTTGA CCAGCGGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC TCCCTCAGCA GGTGGTGAC CGTCCCTCTCC
 CACCTTGAGT CCGCGGGACT GGTCCCGCA CGTGTGAAG GCGCGACAGG ATGTGAGAG TCCTGAGATG AGGGAGTCGT CGCACCACTG GCACGGGAGG
 160 W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S
 1501 AGCAGCTTGG GCACCCAGAC CTACATCTGC AACGTGAATC ACAAGCCAG CAACACCAAG GTCGACAAGA AAGTTGAGCC CAAATCTTGT GACAAAACTC
 TCGTCGAACC CGTGGGCTG GATGTAGACG TTGCACCTAG TGTTGGGTC GTTGTGGTTC CAGCTGTCTT TTCAACTCGG GTTTAGAACA CTGTTTGTAG
 193 S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H
 1601 ACCTCAGTGG CCGTGGCTCT GGTCCGGTG ATTTTGATTA TGAAGAAGATG GCAAACGCTA ATAAGGGGGC TATGACCGAA AATGCCGATG AAAACGGCGT
 TGGAGTCACC GCCACCGAGA CCAAGGCCAC TAAACTAAT ACTTTTCTAC CGTTTGGGAT TATTCGCCG ATACTGGCTT TTACGGCTAC TTTTCCGCGA
 227 L S G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L
 ^end of heavy chain
 ^start of gene III coat protein (267-end)
 1701 ACAGTCTGAC GCTAAAGGCA AACTTGATTC TGTCGCTACT GATTACGGTG CTGTATCGA TGGTTTCATT GGTGACGTTT CCGGCCCTGC TAATGGTAAT
 TGTGAGACTG CGATTTCGT TTGAACAAAG ACAGCGATGA CTAATGCCAC GACGATAGCT ACCAAAGTAA CCACGTGCAA GCGCGGAAG ATTACCATTA
 260 Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N
 1801 GGTGCTACTG GTGATTTTGC TGGCTCTAAT TCCCAATGG CTCAAGTCGG TGACGGTGAT AATTCACCTT TAATGAATAA TTTCCGTCAA TATTACCTT
 CCACGATGAC CACTAAAACG ACCGAGATTA AGGGTTTACC GAGTTCAGCC ACTGCCACTA TTAAGTGGAA ATTACTTATT AAAGGCAGTT ATAAATGGAA
 293 G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S
 1901 CCCTCCCTCA ATCGGTTGAA TGTGCGCCTT TTGTCCTTTAG CGCTGGTAA CCATATGAAT TTTCTATTGA TTGTGACAAA ATAAACTTAT TCCGTGGTGT
 GGGAGGGAGT TAGCCAACCT ACAGCGGGAA AACAGAAATC GCGACCATTT GGTATACTTA AAAGATAACT AACACTGTTT TATTGATA AGCACCAACA
 327 L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V
 2001 CTTTTCGTTT CTTTATATG TTGCCACCTT TATGTATGTA TTTTCTACGT TTGCTAACAT ACTCGGTAAT AAGGAGTCTT AA
 GAAACGCCAA GAAATATAC AACGGTGGAA ATACATACAT AAAAGATGCA AACGATTGTA TGACGCATTA TTCTCAGAA TT
 360 F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 27C

1 ATGAAAAAGA ATAAGGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAT GCCATATGCAG ATATCCAGAT GACCCAGTCC CCGAGCTCCC
 TACTTTTCT TATAGCGTAA AGAAGAAGCT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTC TATAGGTCTA CTGGGTGAGG GGCTCGAGGG
 1 M K K N I A F L L A S M F V F S I A T N A Y A D I Q M T Q S P S S L
 ^met
 ^start of stII signal sequence
 ^start of light chain
 101 TGTCCGCCCTC TGTGGGCGAT AGGTCACCA TCACCTGCCG TGCCAGTCAG GATGTGTCCA CTGCTGTAGC CTGSTATCAA CAGAAACCAG GAAAAGCTCC
 ACAGGCGGAG ACACCCGCTA TCCCAGTGGT AGTGGACGGC ACGGTCAGTC CTACACAGGT GACGACATCG GACCATAGTT GTCTTTGGTC CTTTTCGAGG
 35 S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A P
 ^CDR-L1
 201 GAAGCTTCTG ATTTACTCGG CATCCTTCCT CTACTCTGGA GTCCCTTCTC GCTTCTCTGG TAGGGGTTCC GGGAGGATT TCACCTCTGAC CATCAGCAGT
 CTTGGAAGAC TAAATGAGCC GTAGGAAGGA GATGAGACCT CAGGGAAGAG CGAAGAGACC ATCGCCAAGG CCCTGCCTAA AGTGAGACTG GTAGTCGTCA
 68 K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S S
 ^CDR-L2
 301 CTGCAGCCGG AAGACTTCG AACTATTAC TGTGAGGAC ATTATACTAC TCCTCCACG TTCGGACAGG GTACCAAGGT GGAGATCAA CGAACTCTGG
 GACGTCGGCC TTCTGAAGCG TTGAATAATG ACAGTCCTTG TAATATGATG AGGAGGTCG AAGCCTGTCC CATGGTTCCA CCTTAGTTT GCTTGACACC
 101 L Q P E D F A T Y Y C Q Q H Y T T P P T F G Q G T K V E I K R T V A
 ^CDR-L3
 401 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGACCA GTTGAAATCT GGAACCTGCT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC
 GACGTGGTAG ACAGAAGTAG AAGGCGGTA GACTACTCGT CAACTTTAGA CCTTGACGGA GACAACACAC GGACGACTTA TTGAAGATAG GGTCTCTCCG
 135 A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A
 501 CAAAGTACAG TGAAGGTGG ATAAAGCCCT CCAATCGGT AACTCCAGG AGAGTGTAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC
 GTTTCATGTC ACCTTCCACC TATTGCGGA GTTACGCCA TTGAGGGTCC TCTCACAGTG TCTCGTCTCTG TCGTTCTCTGT CGTGGATGTC GGAGTCGTGG
 168 K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S
 601 ACCCTGACGC TGAGCAAAAGC AGACTACGAG AAACACAAAG TCTACGCGTG CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA
 TGGGACTGCG ACTCGTTTCG TCTGATGCTC TTTGTGTTTC AGATGCGGAC GCTTCAGTGG GTAGTCCCGG ACTCGAGCGG GCAGTGTTC TCAGAGTTGT
 201 T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R

FIG. 28A

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701 GGGGAGAGTG TGGTGCCAGC TCCGGTATGG CTGATCCGAA CCGTTTCCGC GGTAAAGGACC TGGCATAAAT CGAGGCTGAT CCTCTACGCC GGACGCATCG
    CCCCTCTCAC ACCACGGTCG AGGCCATACC GACTAGGCTT GGCAAGGCG CCATTCTGG ACCGTATTGA GCTCCGACTA GGAGATGCGG CCTGCGTAGC
235 G E C G A S S G M A D P N R F R G K D L A O
    ^end of light chain, start of gD tag

801 TGGCCCTAGT ACGCAAGTTC ACGTAAAAAG GGTAACTAGA GGTGAGGTG ATTTTATGAA AAGAATATC GCATTCTTC TTGCACTAT GTTCGTTTTT
    ACCGGGATCA TCGGTTCAAG TGCATTTTTC CCATTGATCT CCAACTCCAC TAAAAACTT TTCTTTATAG CGTAAAGAAG AACGTAGATA CAAGCAAAAA
-23      M K K N I A F L L A S M F V F
    ^start of stII

901 TCTATTGCTA CAAACGCGTA CGCTGAGGTT CAGCTGGTGG AGTCTGGCGG TGGCTGGTG GCTCACTCCG TTTGTCTGT GCAGCTTCTG
    AGATAACGAT GTTTCGGCAT GCGACTCCAA GTCGACCACC TCAGACCGCC ACCGGACCC GTCGGTCCCC CGAGTGAGGC AAACAGGACA CGTCGAAGAC
-8 S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S G
    ^start of heavy chain          ^CDR-H1

101 GCTTCACCAT TAGTAATTAT GGGATACACT GGGTGGGTCA GGGCCCGGGT AAGGGCTGG TAGGATTCT CCTTCTAAGC GCTCTACTTA
    CGAAGTGGTA ATCATTAATA CCTATGTGA CCCACGCACT CCGGGGCCCA TTCCCGGACC TTACCCAACC ATCTAAAGA GGAAGATTGC CGAGATGAAT
27 F T I S N Y G I H W V R Q A P G K G L E W V G R I S P S N G S T Y
    ^CDR-H2

101 CTATGCCCGAT AGCGTCAAGG GCGGTTTCAC TATAAGCGCA GACACATCCA AAAACACAGC CTACCTACAA ATGAACAGCT TAAGAGCTGA GGACACTGCC
    GATACGGCTA TCGCAGTTCC CGGCAAGTG ATATTCCGGT CTGTGTAGGT TTTGTGTGCG GATGGATGT TACTGTGCGA ATTCTCGACT CCTGTGACGG
60 Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T A

201 GTCTATTATT GTGCAAAATG CTCGGTCAGG TTCGGTTACT GGGGTCAAGG AACACTAGTC ACCGTCTCCT CGGCCTCCAC CAAGGCCCA TCGGTCTTCC
    CAGATAATAA CAGGTTTAC GAGCCAGTCC AAGCGAATGA CCCCAGTTCC TTGTGATCAG TGGCAGAGGA GCCGGAGGTG GTTCCCGGGT AGCCAGAAGG
93 V Y Y C A K C S V R F A Y W G Q G T L V T V S S A S T K G P S V F P
    ^CDR-H3

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FIG. 28b

101 CCCTGGCACC CTCCTCCCAAG AGCACCTCTG GGGGCACAGC GGGCCTGGGC TGCCCTGGTCA AGGACTACTT CCCCAGAACG GTGACGGTGT CGTGGAACTC
 GGGACCGTGG GAGGAGGTTT TCGTGGAGAC CCCCCTGTTCG CCGGGACCCG ACGGACCACT TCGTGATGAA GGGGCTTGGC CACTGCCACA GCACCTTGAG
 27 L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V S W N S
 .01 AGCGGCCCTG ACCAGCGGCG TGCACACCTT CCGGCTGTCT CTACAGTCTT CAGGACTCTA CTCCCTCAGC AGCGTGGTGA CCGTGCCCTC CAGCAGCTTG
 TCCGCGGGAC TGGTCCCGC ACGTGTGAA GGGCCGACAG GATGTGAGG GATGTGAGG GAGGAGTGC TCGCACCCTT GGCACGGGAG GTGCTGGAAC
 60 G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S S S L
 01 GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGACAAAG AAGTTGAGC CCAATCTTG TGACAAAAC CACCTCAGTG
 CCGTGGGTCT GGATGTAGAC GTTGCACTTA GTGTGCGGT GTGTGCGGT CCAGCTGTTT CAGCTGTTTGA ACTGTTTGA GTGGAGTCA
 93 G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T H L S G
 start of gene III coat protein (267-end)
 ^end of heavy chain
 01 GCGGTGGCTC TGGTTCGGT GATTTTGATT ATGAAAAGAT GGCAAAACGT AATAAGGGG CTATGACCGA AATGCGCAT GAAAACGGC TACAGTCTGA
 CGCCACCGAG ACCAAGGCCA CTAATACTAA TACTTTCTA CCGTTTGGG TTTATCCCC GATCTGGCT TTTACGGCTA CTTTGGCGG ATGTCAGACT
 27 G G S G S G D F D Y E K M A N A N K G A M T E N A D E N A L Q S D
 01 CGCTAAAGGC AAATCTGATT CTCTCGCTAC TGATTACGGT GCTGCTATCG ATGTTTCTAT TGGTGACGTT TCCGGCCTTG CTAATGGTAA TGGTGCTACT
 GCGATTCCG TTGGAACCTA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAAGTA ACCACTGCAA AGGCGGAAC GATTACCATT ACCACGATGA
 60 A K G K L D S V A T D Y G A A I D G F I G D V S G L A N G N G A T
 01 GGTGATTITG CTGCTCTAA TTCCCAAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCGTCA ATATTACCT TCCCTCCCTC
 CCACTAAAC GACCGAGATT AAGGTTTAC CGAGTTCAGC CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGCAGT TATAAATGA AGGAGGGAG
 93 G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S L P Q
 01 AATCGGTGA ATGTGCGCCT TTTGTCTTTA GGGCTGGTAA ACCATATGA TTTTCTATTG ATTGTGACAA AATAAACTTA TTCCGTGGTG TCTTTGCGTT
 TTAGCCAACT TACAGCGGA AAACAGAAAT CCGGACCATT TGGTATACCT AAAAGATAAC TAACACTGTT TTAATTGAAT AAGCACCAC AGAAACGCAA
 27 S V E C R P F V F S A G K P Y E F S I D C D K I N L F R G V F A F
 01 TCTTTTATAT GTTCCACCT TTAATGATGT ATTTTCTACG TTTGCTTACA TACTGCGTAA TAAGAGTCT TAA
 AGAAATATA CAACGGTGA AATACATACA TAAAGATGC AAACGATGT ATGACCAT ATTCCCTCAGA ATT
 60 L L Y V A T F M Y V F S T F A N I L R N K E S O

37/75

FIG. 28C

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCCG TTTTTCAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
 TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTA CGGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
 1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
 ^met
 ^start of stII signal sequence
 ^light chain start
 101 CCCTGTCCGC CTCGTGGGC GATAGGTTCA CCATCACCTG CCGTSCCAGT CAGGATGTGT CCACGTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
 GGGACAGGCG GAGACACCCG CTATCCCACT GGTAGTGGAC GGCACGGTCA GTCTACACA GGTGACGACA TCGGACCATA GTTGCTTTTG GTCCTTTTCG
 35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
 ^CDR-L1
 201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTTACTCTT GGAGTCCCTT CTGCTTCTC TGGTAGCGGT TCCGGGACGG ATTCACTCT GACCATCAGC
 AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGA GAGCAAGAG ACCATCGCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
 68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S
 ^CDR-L2
 301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCTCC ACCTTCGGAC AGGGTACCAA GGTGGAGATC AAACGAATG
 TCAGACGTCG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TCGAAGCCTG TCCATGGTT CCACCTCTAG TTTGCTTAC
 101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
 ^CDR-L3
 401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACCTG CCTCTGTTGT GTGCTGCTG AATAACTTCT ATCCCAGAGA
 ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATGAAGA TAGGCTCTCT
 135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E
 501 GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCAATCG GGTAACTCC AGGAGAGTGT CACAGAGCAG GACAGCAAG ACAGACCTA CAGCCTCAGC
 CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTAGC CCATTGAGG TCTCTCACA GTGTCTCGTC CTGCTGTTCC TGTCGTGGAT GTCGGAGTCG
 168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S
 601 AGCACCTTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCATCAGG GCCTGAGTTC GCCCGTCACA AAGAGCTTCA
 TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATGCG GACGCTCAG TGGGTAGTCC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT
 201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

FIG.- 29 A

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11 ACAGGGGAGA GTGTGTTGCC AGCTCCGGTA TGCTGATCC GAACGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
TGTCCCTCTCT CACACACAGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CCGGCTGCGT
15 R G E C G A S S G M A D P N R F R G K D L A O
^end of light chain, start of gD tag

11 TCGTGGCCCT AGTACGCAAG TTCACGTAAG AAGGGTAACT AGAGGTTGAG GTGATTTTAT GAAAAAGAAT ATCGCATTTT TTCTTGCAATC TATGTTTCGTT
AGCACCGGGA TCATGGGTTTC AAGTGCAATTT TTCCCATTTGA TCTCCAACTC CACTAAATAA CTTTTCCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
13 M K K N I A F L L A S M F V
^start of stII

11 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CCGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGCTC TGTGCAGCTT
AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CACGTCGTC CCCCAGATGA GGCAAAACAGG ACACGTCGAA
19 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S
^start of heavy chain ^CDR-H1

11 CTGGCTTCAC CATTAGTGGT TCTGATATAC ACTGGGTGCG TCAGGCCCCG GGTAAAGGCC TGGTAAAGGTT TGTAGGATT TCTCCTTATG GCGGCAATAC
GACCGAAGTG GTAATCACCA AGACTATATG TGACCCACGC AGTCCGGGGC CCATTCCCG ACCTTACCCA ACCATCTCTAA AGAGGAATAC CGCCGTTATG
39/75 6 G F T I S G S D I H W V R Q A P G K G L E W V G R I S P Y G G N T
^CDR-H2

11 TAACTATGCC GATAGCGTCA AGGCCCGTTT CACTATAAGC GCAGACACAT CCATAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
ATTGATACGG CTATCGCAGT TCCCGGGCAA GTGATATTTCG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
19 N Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

11 GCCGTCTATT ATTGTGCAAG AGTCGGCGGC CTCAAGTTGC TGTTCGACTA CTGGGGTCAA GGAACACTAG TCACCGCTCTC CTCGGCCCTCC ACCAAGGGCC
CGGCAGATAA TAACACGTTT TCAGCCGCGG GAGTTCAACG ACAAGCTGAT GACCCAGTT CATTCTGATC AGTGGCAGAG GAGCCGAGG TGGTTCCCGG
2 A V Y Y C A R V G G L K L L F D Y W G Q G T L V T V S S A S T K G P
^CDR-H3

11 CATCGGTCTT CCCCTTGGCA CCTCTCTCCA AGAGCACCTC TGGGGGCACA GGGGCCCTGG GTTCCCTGGT CAAGGACTAC TTCCCCGAAC CCGTGACGGT
GTAGCCAGAA GGGGGACCGT GGGAGGAGGT TCTCGTGGAG ACCCCCGTGT CCGCGGGACC CGAGGGACCA GTTCTGTATG AAGGGGCTG GCCACTGCCA
6 S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T V

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FIG. 29B

1401 GTGCTGGAAC TCAGGGGCCC TGACCAGCGG CGTGCACACC TTCCGGCTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGET GACCGTGCCC
 CAGCACCTTG AGTCCGGGGG ACTGCTCGCC GCACGTGTGG AAGGCCGAC AGGATGTCAG GAGTCTCTGAG ATGAGGGAGT CGTCGCCACCA CTGGCACGGG
 159 S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P
 1501 TCCAGCAGCT TGGGACCCCA GACCTACATC TGCAACGTGA ATCACAAGCC CAGCAACACC AAGGTCGACA AGAAAGTTGA GCCCAAATCT TGTGACAAAA
 AAGTCGTGCA ACCCGTGGT CTGGATGTAG ACGTTGCACT TACGTGTCGG GTCTGTGTTGG TTCCAGCTGT TCTTTCAACT CGGGTTTAGA ACACCTGTTTT
 192 S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K T
 1601 CTCACGGCGC CATGAAACAG CTAGAGGACA AGGTGGAAGA GCTACTCTCC AAGAACTACC ACCTAGAGAA TGAAGTGGA AGACTCAAAA AACTTGTCTGG
 GAGTGCCGGC GTACTTTGTC GATCTCCTGT TCCAGCTTCT CGATGAGAGG TTCTTGTATGG TGGATCTCTT ACTTCACCGT TCTGAGTTTT TTGAACAGCC
 226 H G R M K Q L E D K V E L L S K N Y H L E N E V A R L K K L V G
 ^end of heavy chain, start of leucine zipper
 1701 GGAGCGCGGA AAGCTTAGTG GCGGTGGCTC TGGTTCGGT GATTITGATT AFGAAGAAGT GGCAACGCT AATAAGGGGG CTATGACCGA AAATGCCGAT
 CCTCGCGCCT TTCGAATCAC CGCCACCCAG ACCAAGGCCA CTAAAACTAA TACTTTTCTA CCGTTTGGCA TTATTCCCCC GATACTGGCT TTTACGGCTA
 259 E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A D
 ^end of leucine zipper, gene III coat protein (267-end)
 1801 GAAAACGCGC TACAGTCTGA CGCTAAAGGC AAACCTTGATT CTCTCGCTAC TGATTACGGT GCTGCTATCG ATGGTTTCAT TGGTGACGTT TCCGGCCCTTG
 CTTTTCGGCG ATGTCAGACT GCGATTTCGG TTTGAACTAA GACAGCGATG ACTAATGCCA CGACGATAGC TACCAGAGTA ACCACTGCAA AGGCCGGAAC
 292 E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L A
 1901 CTAATGGTAA TGGTGTACT GGTGATTTTG CTGGCTCTAA TTCCCAATG GCTCAAGTCG GTGACGGTGA TAATTCACCT TTAATGAATA ATTTCCTGCA
 GATTACCAT ACCACGATGA CCACCTAAAC GACCGAGATT AAGGTTTAC CGACTTCAGC CACTGCCACT ATTAAGTGA AATTACTTAT TAAAGGCAGT
 326 N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R Q
 2001 ATATTACCT TCCTCCCTC AATCGGTTGA ATGTCGCCCT TTTGTCTTTA GCGGTGGTAA ACCATATGAA TTTTCTATTG ATTGTGACAA AATAAACCTTA
 TATAAATGGA AGGAGGGGAG TTAGCCCACT TACAGCGGGA AAACAGAAAT CCGGACCATT TGGTATACTT AAAAGATAAC TAACACTGTT TTATTGTAAT
 359 Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N L
 2101 TTCCGTGGTG TCTTTGCGTT TCTTTTATAT GTTGCCACCT TTATGTATGT ATTTTCTACG TTTGCTAACA TACTGCGTAA TAAGGAGTCT TAA
 AAGGCACCAC AGAAACGCAA AGAAATATA CAACGGTGA AATACATACA TAAAGATGC AAACGATTGT ATGACGCATT ATTCCTCAGA ATT
 392 F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 29C


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1 ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAT GCCTATGCGT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATCTTAA CCGATACGTA GGCTATAGGT CTACTGGGTC AGGGGCTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^start of stII signal sequence
^met
^light chain start

101 CCCTGTCCGC CTCTGTGGGC GATAGGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTGT CCACGTCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
GGGACAGGCG GAGACACCCG CTATCCCACT GGTAGTGGAC GGCACGGTCA GTCTACACA GGTGAGGACA TCGGACCATA GTTGTCTTTG GTCTTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTACT CGGCATCCTT CCTCTACTCT GGAGTCCCTT CTGCTTCTC TGCTAGCGGT TCCGGGACGG ATTTCACTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA GGAGATGAGA CCTCAGGGA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGGTAGTCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCTCTCC AGTTCGGAC AGGTACCAA GGTGAGATC AAACGAACTG
TCAGACGTGG GCCTTCTGAA GCGTTGAATA ATGACAGTCG TTAGAATATG ATGAGGAGGG TGCAAGCCTG TCCCATGGTT CCACCTCTAG TTTGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAACTG CCTCTGTTGT GTGCTGTCTG AATAACTTCT ATCCAGAGA
ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGCTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGGAGG TGGATAACGC CCTCCAATCG GGTAACCTCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG TCCTCTCACA GTGCTCTGTC CTGCTGTTCC TGTCGTGGAT GTCGGAGTCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCATCAGG GCCTGAGTC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTGT TTCAGATCGG GACGCTTCAG TGGTAGTCC CCGACTCAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG. 30A

701 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
 TGTCCCTCT CACACCACGG TCGAGGCCAT ACCGACTAGG CTTGGCAAG GCGCATTC TGGACCGTAT TGAGCTCCGA CTAGAGATG CGGCTCGGT
 35 R G E C G A S S G M A D P N R F R G K D L A O
 ^end of light chain, start of gD tag

 101 TCGTGGCCCT AGTACGCAAG TTCACGTAAG AAGGGTAACT AGAGTTGAG GTGATTTTAT GAAAAAGAT ATCGCATTC TTCTTGCATC TATGTTCTGT
 AGCACCGGGA TCATGCGTTC AAGTGCATTT TTCCCATTTGA TCTCCAACTC CACTAATAA CTTTTTCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
 23 M K K N I A F L L A S M F V
 ^start of still

 01 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CGGTGGCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT
 AAAAGATAAC GATGTTTGG CATGCGACTC CAAGTCGACC ACCTCAGACC GCCACCGGAC CAGCTCGGTC CCCCGAGTGA GGCACACAGG ACACGTCGAA
 -9 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S
 ^start of heavy chain

 01 CTGGCTTCAC CATTACTAAT TCCGATATAC ACTGGTGCG TCAGGCCCGG GGTAAAGGCC TGAATGGGT TGCTACTATT TATCCTTATG GCGGCTATAC
 GACGGAAGTG GTAATGATTA AGGCTATATG TGACCCAGCG AGTCCGGGCG CCATTCCCGG ACCTTACCCA AGCATGATAA ATAGAATAC CGCCGATATG
 6 G F T I T N S D I H W V R Q A P G K G L E W V A T I Y P Y G G Y T
 ^CDR-H2

 11 TTACTATGCC GATAGGCTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAACAC AGCCTACCTA CAAATGAACA GCTTAAGAGC TGAGGACACT
 AATGATACGG CTATCGCAGT TCCCGGCATA GTGATATTGC CGTCTGTGTA GGTCTTGTG TCGGATGGAT GTTTACTTGT CGAATCTCTG ACTCCTGTGA
 19 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T

 1 GCCGTCTATT ATTGTGCAAG AGGGGGCGG ATGGACGGCT AGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCTCGGCC TCCACCAAGG
 CGGCAGATAA TAACACGTTT TCCCGCGCC TACCTGCCGA TGCAATACCT GATGACCCCA GTTCTTGTG ATCAGTGGA GAGGAGCCG AGGTGGTTCC
 2 A V Y Y C A R G G G M D G Y V M D Y W G Q G T L V T V S S A S T K G
 ^CDR-H3

 1 GCCCATCGGT CTTCCCCCTG GCACCTCTCT CCAAGAGCAC CTCTGGGGG ACAGGGGCC TGGGTGCTT GGTCAAGGAC TACTTCCCCG AACCGGTGAC
 CGGTAGCCA GAAGGGGAC CGTGGGAGGA GGTCTCGTG GAGACCCCG TGTCCCGCGG ACCCGACGGA CCAGTCTCTG ATGAAGGGG TTGGCCACTG
 6 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

FIG. 30b

1401 GGTGTCGTGG AACTCAGGCG CCCTGACCAG CGGCGTGCAC ACCTTCCCGG CTGTCTTACA GTCTACTCCC TCAGCAGCGT GGTGACCGTG
 CCACAGCAC TTTAGTCCGC GGGACTGGTC GCGGCACGTG TGGAGGGCC GACAGGATGT CAGGAGTCCT GAGATGAGG AGTCGTGCA CCACTGGCAC
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V
 1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACA GCCCAGCAAC ACCAAGTGG ACAAGAAAGT TGAGCCCAA TCTTGTGACA
 GGGAGGTCGT CGAACCCGTG GGTCTGGATG TAGACGTTC ACTTAGTGT CGGGTCGTG TGGTTCAGC TGTCTCTTCA ACTCGGGTTT AGAACACTGT
 192 P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K
 1601 AAACCTCAGG CCGCATGAAA CAGCTAGAG ACAAGTTCG AGAGCTACTC TCCAAGAACT ACCACCTAGA GAATGAAGT GCAAGACTCA AAAAAGTTGT
 TTTGAGTGCC GCGGTACTTT GTCGATCTCC TGTTCAGCT TCTCGATGAG AGGTCTCTGA TGGTGGATCT CTTACTTCAC CGTCTCTGAG TTTTGAACA
 226 T H G R M K Q L E D K V E L L S K N Y H L E N E V A R L K K L V
 'end of heavy chain, start of leucine zipper
 1701 CGGGGAGCGG GGAAGCTTA GTGGCGGTGG CTCTGGTTCC GGTGATTTTG ATTATGAAA GATGGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCC
 GCCCTCGCG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATATATCC CCCGATCTG GCTTTTACGG
 259 G E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A
 'end of leucine zipper, start of gene III coat protein (267-end)
 801 GATGAAAACG CGCTACAGTC TGACGCTAAA GGCAAACTTG ATTCGTGTCG TACTGATTAC GGTCTGCTA TCGATGGTTT CATGTGGTGAC GTTTCGGGCC
 CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAA GTAACCACTG CAAAGGCCGG
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L
 1901 TTGCTAATGG TAAFGGTGCT TTGCTGGCTC TAATTCOCOA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTTAATGA ATAAATTCGG
 AACGATTACC ATTACACGA TGACCACCTAA AAGACCGAG ATTAAGGTT TACCGAGTTC AGCCACTGCC ACTATTAGT GGAAATTAAT TATTAAAGGC
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R
 2001 TCAATATTTA CCTCCCTCC CTCAATCGGT TGAATGTGC CCTTTTGTCT TTAGCGGTGG TAAACCAAT GAATTTTCTA TTGATTTGTA CAAAATAAAC
 AGTTATAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAACACAGA AATCGGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTG
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N
 2101 TTATTCCGCG GTGTCTTTTG GTTCTCTTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACCTTTGCTA ACATACCTGG TAATAAGGAG TCTTAA
 AATAAGGCAC CACAGAAAACG CAAAGAAAAT ATACAACGGT GGAATATACAT ACATAAAGA TGCAACGAT TGTATGACCG ATTATTCTC AGAATT
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 30C

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1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTTCCTAT TGCTACAAAT GCCTATGCAT CCGATATCCA GATGACCCAG TCCCCGAGCT
TACTTTTCTT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAGATA ACATGTTTA CCGATACGTA GGCTATAGGT CTACTGGGTC AGGGGTCGA
1 M K K N I A F L L A S M F V F S I A T N A Y A S D I Q M T Q S P S S
^met ^light chain start

101 CCCTGTCCGC CTCTGTGGC GATAGGTCA CCATCACCTG CCGTGCCAGT CAGGATGTTT CCACTGCTGT AGCCTGGTAT CAACAGAAAC CAGGAAAAGC
GGGACAGCG GAGACACCCG CTATCCAGT GGTAGTGGAC GGCACGGTCA GTCCTACACA GGTGACGACA TCGGACCATA GTTGTCTTTG GTCTTTTTCG
35 L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K P G K A
^CDR-L1

201 TCCGAAGCTT CTGATTTACT CCGCATCCCTT CCTCTACTCT GGAGTCCCTT CTCGGCTTCTC TGGTAGCGGT TCCGGGACGG ATTCACTCT GACCATCAGC
AGGCTTCGAA GACTAAATGA GCCGTAGGAA CCGATGAGA GGAGATGAGA CCTCAGGAA GAGCGAAGAG ACCATCGCCA AGGCCCTGCC TAAAGTGAGA CTGCTAGTCCG
68 P K L L I Y S A S F L Y S G V P S R F S G S G T D F T L T I S
^CDR-L2

301 AGTCTGCAGC CGGAAGACTT CGCAACTTAT TACTGTGAGC AATCTTATAC TACTCCCTCC ACCTTCGGAC AGGTACCAA GGTGGAGATC AAACGAACTG
TCAGACGTGC GCCTTCGAA GCGTTGAAAT ATGACAGTGC TTAGAATATG ATGAGGAGGG TGCAAGCTG TCCCATGGTT CCACCTCTAG TTGCTTGAC
101 S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E I K R T V
^CDR-L3

401 TGGCTGCACC ATCTGTCTTC ATCTTCCGC CATCTGATGA GCAGTTGAAA TCTGGAATG CCTCTGTTGT GTGCCCTGCTG AATAACTTCT ATCCCAGAGA
ACCGACGTGG TAGACAGAAG TAGAAGGGCG GTAGACTACT CGTCAACTTT AGACCTTGAC GGAGACAACA CACGGACGAC TTATTGAAGA TAGGGTCTCT
135 A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E

501 GGCCAAAGTA CAGTGAAGG TGGATAACG CCTCCAATCG GGTAACTCC AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC
CCGGTTTCAT GTCACCTTC ACCATTGCG GGAGGTTAGC CCATTGAGG TCCTCTCACA GTGTCTCGTC CTGTCTGTTCC TGTCGTGGAT GTCGGAGTCCG
168 A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S

601 AGCACCCCTGA CCGTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA
TCGTGGGACT GCGACTCGTT TCGTCTGATG CTCTTTGTTG TTCAGATGG GACCTTCAG TGGGTAGTCC CCGACTCGAG CGGGCAGTGT TTCTCGAAGT
201 S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N

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FIG. 31A

11 ACAGGGGAGA GTGTGGTGCC AGCTCCGGTA TGGCTGATCC GAACCGTTTC CGCGGTAAGG ACCTGGCATA ACTCGAGGCT GATCCTCTAC GCCGGACGCA
 TGTCCCTCTT CACACACAGG TCGAGGCCAT ACCGACTAGG CTTGGCAAAG GCGCCATTCC TGGACCGTAT TGAGCTCCGA CTAGGAGATG CCGCCTGCGT
 15 R G E C G A S S G M A D P N R F R G K D L A O
 ^end of light chain, start of gD tag
 11 TCGTGGCCCT AGTACGCAAG TTCACGTAAA AAGGGTAACT AGAGGTGAG GTGATTTTAT GAAAAAGAAAT ATCGCATTTT TTCTTGCAATC TATGTTGCTT
 AGCACCGGGA TCATGGCTTC AAGTGCAATT TTCCCATTTA TCTCCAACTC CACTAAAATA CTTTTCCTTA TAGCGTAAAG AAGAACGTAG ATACAAGCAA
 13 M K K N I A F L L A S M F V
 ^start of still
 1 TTTTCTATTG CTACAAACGC GTACGCTGAG GTTCAGCTGG TGGAGTCTGG CCGTGGCCCTG GTGCAGCCAG GGGGCTCACT CCGTTTGCTC TGTGCAGCTT
 AAAAGATRAA GATGTTTGG CATGGGACTC CAAGTCGACC ACCTCAGACC GCCACGGGAC CACGTCGGTC CCCCAGGTGA GGCAACACAGG ACACGTCGAA
 9 F S I A T N A Y A E V Q L V E S G G L V Q P G G S L R L S C A A S
 ^start of heavy chain ^CDR-H1
 1 CTGGCTTCAC CATTAATAAT TATGATATAC ACTGGGTGCG TCAGGCCCGG GGTAAAGGCC TGGATGGGT TGGTTATATT TCTCCTCCTA GCGGGCTAC
 GACCGAAGTG GTAATTATTA ATACTATATG TGACCCACGC AGTCCGGGGC CCATTCCCGG ACCTTACCCA ACCAATATAA AGAGGAGGAT CGCCGCGATG
 45/75 ; G F T I N N Y D I H W V R Q A P G K G L E W V G Y I S P P S G A T
 ^CDR-H2
 1 TTACTATGCC GATAGCGTCA AGGGCCGTTT CACTATAAGC GCAGACACAT CCAAAAACAC AGCTACCTA CAAATGAACA GCTTAAAGAC TGAGGACACT
 AATGATACGG CTATCGCAGT TCCCGGCAAA GTGATATTG CGTCTGTGTA GGTTTTGTG TCGGATGGAT GTTTACTTGT CGAATTCTCG ACTCCTGTGA
 9 Y Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E D T
 1 GCCGTCTATT ATTGTGCAAG AATGTCGGC ATGCGGAGGG GGGTTATGGA CTACTGGGGT CAAGGAACAC TAGTCACCGT CTCTCGGGCC TCCACCAAGG
 CGGCAGATAA TAACACGTTT TTACCAGCCG TAGCCCTCCC CCAATACCT GATGACCCCA GTTCCTTGTG ATCAGTGGCA GAGGAGCCGG AGGTGTTCC
 2 A V Y Y C A R M V G M R R G V M D Y W G Q G T L V T V S S A S T K G
 ^CDR-H3
 1 GCCCATCGGT CTTCCTCCCTG GCACCTCTCT CCAAGAGCAC CTCTGGGGC ACAGGGGCC TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC
 CGGTACCCA GAAGGGGGAC CGTGGGGAGG GGTTCGTGTG GAGACCCCG TGTCCCGGG ACCCGACGGA CCAGTTCCTG ATGAAGGGGC TTGGCCACTG
 6 P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P V T

FIG.-31B

1401 GGTGTCTGG AACTCAGCG CCCTGACCAG CGGCGTGAC ACCTTCCCG CTGTCTTACA GTCTACTCCC TCAGACGCGT GGTGACCGTG
 CCACAGCACC TTGAGTCCGC GGGACTGTC GCGGCACGTG TGAAGGGCC GACAGGATGT CAGGAGTCT GAGATGAGG AGTCGTGCA CCACTGGCAC
 159 V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V
 1501 CCCTCCAGCA GCTTGGGCAC CCAGACCTAC ATCTGCAACG TGAATCACA GCCAGCAAC ACCAAGTGC ACAAGAAAGT TGAGCCCCAA TCTTGTGACA
 GGGAGGTCTG CGAACCCTGT GGTCTGGATG TAGACGTTGC ACTTAGTGT CCGGTCTGTG TGGTCCAGC TGTCTCTTCA ACTCGGGTTT AGAACACTGT
 192 P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S C D K
 1601 AAACCTCAGG CCGCATGAAA CAGCTAGAGG ACAAGGTGCA AGAGCTACTC TCACAAGACT ACCACCTAGA GAATGAAGTG GCAAGACTCA AAAAAGTTGT
 TTTGAGTGCC GCGGTACTTT GTGATCTCC TGTTCAGCT TCTCGATGAG AGGTCTTGA TGGTGGATCT CTTACTTCAC CGTCTGAGT TTTTGAACA
 226 T H G R M K Q L E D K V E L L S K N Y H L E N E V A R L K K L V
 ^end of heavy chain, start of leucine zipper
 1701 CGGGGAGCG GGAAGCTTA GTGGCGTGG CTCTGTTCC GGTGATTTG ATTATGAAA GATGGCAAAC GCTAATAAGG GGGCTATGAC CGAAAATGCG
 GCCCTCGCG CCTTTCGAAT CACCGCCACC GAGACCAAGG CCACATAAAC TAATACTTTT CTACCGTTTG CGATTATTC CCCGATACTG GCTTTTACGG
 259 G E R G K L S G G S G S G D F D Y E K M A N A N K G A M T E N A
 ^end of leucine zipper
 ^gene III coat protein (267-end)
 1801 GATGAAAACG CGCTACAGTC TGACGCTAA GGCAAACTTG ATCTGTGCG TACTGATTAC GGTGCTGCTA TCGATGTTT CATTTGGTGAC GTTTCGGGCC
 CTACTTTTGC GCGATGTCAG ACTGCGATTT CCGTTTGAAC TAAGACAGCG ATGACTAATG CCACGACGAT AGCTACCAAA GTAACCACTG CAAAGGCCGG
 292 D E N A L Q S D A K G K L D S V A T D Y G A A I D G F I G D V S G L
 1901 TTGCTAATGG TAATGGTGT ACTGGTGATT TTGCTGGCTC TAATFCCCAA ATGGCTCAAG TCGGTGACGG TGATAATTCA CCTTTAATGA ATAAATTTCCG
 AACGATTACC ATTACACGA TGACCACCTAA AACGACCGAG ATTAAGGTTT TACCGAGTTC AGCCACTGCC ACTATTAACT GGAATTAAGT TATTAAAGGC
 326 A N G N G A T G D F A G S N S Q M A Q V G D G D N S P L M N N F R
 2001 TCAATATTTA CCTTCCCTCC CTCAATCGGT TGAATGTGCG CCTTTGTCT TTAGCGGTGG TAAACCATAT GAATTTTCTA TTGATTGTGA CAAAATAAAC
 AGTTATAAAT GGAAGGGAGG GAGTTAGCCA ACTTACAGCG GGAATAACAGA AATCGCGACC ATTTGGTATA CTTAAAAGAT AACTAACACT GTTTTATTG
 359 Q Y L P S L P Q S V E C R P F V F S A G K P Y E F S I D C D K I N
 2101 TTATTCCGTG GTGTCTTTGC GTTTCCTTTA TATGTTGCCA CCTTTATGTA TGTATTTTCT ACCTTTGCTA ACATACGCG TAATAAGGAG TCTTAA
 AATAAGGCAC CACAGAAACG CAAAGAAAAT ATACAACGGT GGAATACAT ACATAAAGA TGCAACGAT TGTATGAGC ATTATTCCCTC AGAATT
 392 L F R G V F A F L L Y V A T F M Y V F S T F A N I L R N K E S O

FIG. 31c

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1  GAAATCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAATATC TCATTGGCTGA GTTGTATTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT
   CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGTCTG TACTTTTATAG AGTAACGACT CAACAATAAA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATATG TCGCAATATG GCGCAAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG
   CTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTGCG CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCATTCCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA
   CCGCGGACAT GCTCCATCTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCACAA GCTGTCTATA AGTTGTACAG GCCGAGACTT ATAGTCGGTT TGTTTTATTT TTTTAATGTA TTTGTAACTA GTACGCAAGT
   TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAAA AAAATTACAT AAACATTGAT CATCGGTTCA

401 TCACGTAATA AGGCTATGTA GAGTTTGAGG TGATTTTATG AAAAAGAATA TCGCAATCTT TCTTGCATCT ATGTTTCGTTT TTTCTATTGC TACAAATGCC
   AGTGCATTTT TCCCATACAT CTCCAACCTC ACTAAAATAC TTTTCTTAT AGCGTAAAGA AGAACGTAGA TACAAGCAAA AAAGATAACG ATGTTTACGG

0      M K K N I A F L L A S M F V F S I A T N A
      ^start of stII signal sequence

501 TATGCAGATA TCAGATGAC CCAGTCCCGG AGCTCCCTGT CCGCTCTGT GGGCATAGG GTCACCATCA CCTGCCCTGC CAGTCAGGAT GTGTCCACTG
   ATACGTCTAT AGGTCTACTG GGTGAGGGG TCGAGGGGACA GGGGAGACA CCGGTATCC CAGTGTAGT GGACGGCAGG GTCAGTCCCTA CACAGGTGAC
21 Y A D I Q M T Q S P S S L S A S V G D R V T I T C R A S Q D V S T A
      ^start of light chain
      ^EcorV
      ^CDR-L1

601 CTGTAGCCTG GTATCAACAG AAACCAGGAA AAGCTCCGAA GCTTCTGATT TACTCGGCAT CCTTCTCTTA CTCTGGAGTC CCTTCTCGCT TCTCTGGTAG
   GACATCGGAC CATAGTTGTC TTTGGTCTTT TTTCGAGGCTT CGAAGACTAA ATGAGCCGTA GGAAGGAGAT GAGACTCAG GGAAGAGCGA AGAGACCATC
55 V A W Y Q Q K P G K A P K L L I Y S A S F L Y S G V P S R F S G S
      ^CDR-L2

701 CGGTTCCGGG ACGGATTCA CTCGTACCAT CAGCAGTCTG CAGCCGGAAG ACTTCGCAAC TTATTACTGT CAGCAATCTT ATACTACTCC TCCCACGTTT
   GCCAAGGCC TGCCTAAAGT GAGACTGGTA GTCGTACAG GTCGGCCCTC TGAAGCGTTG AATAATGACA GTCGTTAGAA TATGATGAGG AGGTTGCAAG
88 G S G T D F T L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F
      ^CDR-L3

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FIG.-32A

1 GGACAGGGTA CCAAGGTGA GATCAAACGA ACTGTGGCTG CACATCTGT CTTATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
 CCTGTCCCAT GGTTCACCT CTAGTTTGGT TGACACCGAC GTGGTAGACA GAAGTAGAAG GCGGTAGAC TACTCGTCAA CTTTAGACCT TGACGGAGAC
 1 G Q G T K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V
 ^KpnI

1 TTGTGTGCTT GCTGAATAAC TTCTATCCCA GAGAGGCCAA AGTACAGTGG AAGTGGATA ACGCCTCCA ATCGGGTAAC TCCAGGAGA GTGTACACAGA
 AACACACGGA CGACTTATTG AAGATAGGTT CTCTCCGGTT TCATGTCAAC TTCCACCTAT TCGGGAGGT TAGCCATTG AGGGTCTCT CACAGTGTCT
 5 V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E

1 GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAGTCT ACGCCTGCGA AGTACCCCAT
 CGTCTCTGCG TTCCTGTGCT GGTCTCGGA GTCGTCTGG GACTCGGACT CGTTTCGTCT GATGCTCTTT GTGTTTCAGA TCGGACGCT TCAGTGGGTA
 8 Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H

1 CAGGGCTGA GCTGCCCCGT CACAAAGAGC TTCAACAGGG GAGAGTGTGG TGCCAGCTCC GGTATGGCTG ATCCGAACCG TTTCGCGGT AAGGACCTGG
 GTCCCGGACT CGAGCGGCA GTGTTCTCG AAGTTGTCC CTCTCACACC ACGTCTGAGG CCATACCGAC TAGGCTGGC AAAGGCGCA TTCTTGAGC
 Q G L S S P V T K S F N R G E C G A S S G M A D P N R F R G K D L A
 ^end of light chain, start of gD tag

1 CATAACTGA GGCTGATCCT CTACGCCGGA CGCATCGTGG CCCTAGTAGC CAAGTTCACG TAAAAGGGT AACTAGAGGT TGAGGTGATT TTATGAAAAA
 GTATTGAGCT CCGACTAGGA GATGCGGCTT GGTAGCACC GGTCAAGTC ATTTTCCCA TTGATCTCCA ACTCCACTAA AATACITTTT

M K K
 ^start of stII

1 GAATATCGCA TTTCCTCTTG CATCTATGTT CGTTTTTCTT ATTGCTACAA ACGGTACG TGAGTTTCTG CTGGTGGAGT CTGGCGGTGG CCTGTGTCAG
 CTTATAGCGT AAAGAGAAC GTAGATACAA GCAAAAAAGA TAACGATGTT TGCGCATGG ACTCCAAGTC GACCACCTCA GACCGCCACC GGACACGTC
) N I A F L L A S M F V F S I A T N A Y A E V Q L V E S G G G L V Q
 ^start of heavy chain

^BsiWi

FIG. 328


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1401 CCAGGGGGCT CACTCCGTTT GTCCTGTGCA GCTTCTGGCT TCACCATAG TGGTCTTGG ATACACTGGG TGGTCAAGC CCCGGGTAAG GGCCTGGAAT
GGTCCCCCGA GTGAGGCAAA CAGGACACGT CGAAGACCGA AGTGGTAATC ACCAAGAACC TATGTGACCC ACGCAGTCCG GGGCCCATTC CCGGACCTTA
14 P G G S L R L S C A A S G F T I S G S W I H W V R Q A P G K G L E W
^CDR-H1

1501 GGGTTGCTG GATTGCTCCT TATAGCGGG CTACTGACTA TGCCGATAGC GTCAGGGGCC GTTTCACATAT AAGCGCAGAC ACATCCAAAA ACACAGCCTA
CCCAACGAAC CTAACAGAGGA ATATCGCGCG GATGACTGAT ACGGTATCG CAGTCCCGG CAAAGTGATA TTCGCGTCTG TGTAGGTTTT TGTGTCGGAT
48 V A W I A P Y S G A T D Y A D S V K G R F T I S A D T S K N T A Y
^CDR-H2

1601 CCTACAAATG AACAGCTTAA GAGCTGAGGA CACTGCCGTC TATTATTGTG CAAGAGAGGG GGGCTGTGAC TGGGTGTTCG ACTACTGGG TCAAGGAACA
GGATGTTTAC TTGTGGAATT CTCGACTCCT GTGACGGCAG ATAATAACAC GTTCTCTCCC CCCGACATG ACCCACAAGC TGATGACCCC AGTTCCTTGT
81 L Q M N S L R A E D T A V Y Y C A R E G G L Y W V F D Y W G Q G T
^CDR-H3

1701 CTAGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCTCC TCCAAGAGCA CCTCTGGGG CACAGCGGCC CTGGGCTGCC
GATCAGTGGC AGAGGAGCG GAGGTGGTTC CCGGTAGCC AGAAGGGGA CCGTGGGAGG AGGTCTCTGT GGAGACCCCC GTGTGCGCGG GACCCGACGG
114 L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L
^ApaI

1801 TGGTCAAGGA CTACTTCCC GAACGGTGA CGGTGTCTGG GAACTCAGC GGCCTGACCA GCGGGTGCA CACCTTCCC GCTGTCTTAC AGTCCTCAGG
ACCAGTTCCT GATGAAGGG CTTGGCCACT GCCACAGCAC CTTGAGTCCG CGGGACTGGT CGCGCACGT GTGGAAGGC CGACAGGATG TCAGGAGTCC
148 V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G

1901 ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC AGCTTGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCACAGCA CACCAAGGTC
TGAGATGAGG GAGTCGTGC ACCACTGGCA CCGGAGGTGG TCGAACCCGT GGGTCTGGAT GTAGACGTTG CACTTAGTGT TCGGGTCTGT GTGGTTCAG
181 L Y S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V

2001 GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACC TCTAGAGTGG CGGTGGCTCT GGTCCGGTG ATGCTCGGT GCCGCGGGC GTTTTTTATG
CTGTTCTTTC AACTCGGGT TAGAACACTG TTTTGAFTGG AGATCTCACC GCCACCGAGA CCAAGGCCAC TAGAGCCAA CGGCGGCCCG CAAAAATAC
214 D K K V E P K S C D K T H L O

2101 CTAGGCGCG CCTATACCTT GTCTGCCTCC CCGCGTTGCG TCGCGGTGCA TGGAGCCGG CCACCTCGAC CTGAATGGA GCGGCGGCA CCTCGCTAAC
GATCGGCGG GGATATGGA CAGACGGAGG GCGCAACGC AGCGCCACGT ACCTCGGCC ACCTTACCTT CGGCGGCCGT GGAGCGATTG

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FIG. 32C

2201 GGATTCACCA CTCCAAGAAT TGGAGCCAAAT CAATTCCTGCGGAGAACTGT GAATGCGCAA ACCAACCCCTT GGCAGAACAT ATCCATCGCG TCCGCCATCT
 CCTAAGTGGT GAGGTTCCTTA ACCTCGGTTA GTTAAGAAGC CCTCTTGACA CTACCGCGTT TGGTTGGAA CCGTCTTGTA TAGGTAGCGC AGCGGGTAGA

 2301 CCAGCAGCCG CACGCGGCGC ATCTCGGGCA GCGTTGGGTC CTGGCCACGG GTGCGCATGA TCGTGCTCCT GTCGTTGAGG ACCCGGCTAG GCTGGCGGGG
 GGTCTCGGC GTGCGCGCGG TAGAGCCCGT CGCAACCCAG GACCGGTGCC CACCGTACT AGCAGAGGA CAGCAACTCC TGGGCGGATC CGACCGCCCC

 2401 TTGCGTTACT GGTTAGCAGA ATGAATCACC GATACCGGAG CGAAGCTGAA GCGACTGCTG CTGCAAAAACG TCTGCGACCT GAGCAACAAC ATGAATGGTC
 AACGGAATGA CCAATCGTCT TACTTAGTGG CTATGCGCTC GCTTGCACTT CGCTGACGAC GACGTTTTGC AGACGCTGGA CTCGTGTGTTG TACTTACCAG

 2501 TTCGGTTTCC GTGTTTCGTA AAGTCTGGAA AGCGGGAAGT CAGCGCCCTG CACCATTAAG TTCCGGATCT GCATCGCAGG ATGCTGCTGG CTACCCCTGTG
 AAGCCAAAGG CACAAGCAT TTCAGACCTT TGGCCCTTCA GTGCGGGAC GTGGTAATAC AAGCCCTAGA CGTAGCGTCC TACGACGACC GATGGGACAC

 2601 GAACACCTAC ATCTGTATTA ACGAAGCGCT GGCATTGACC CTGAGTGATT TTCTCTCTGGT CCGCGCGCAT CCATACCGCC AGTTGTTTAC CCTCACAACG
 CTTGTGGATG TAGACATAAT TGCTTCGCGA CCGTAAGTGG GACTCACTAA AAGAGACCA GGGCGGGCGTA GGTATGGCGG TCAACAATG GGAGTGTGTC

 2701 TTCCAGTAAC CGGGCATGTT CATCATCAGT AACCCGTATC GTGAGCATCC TCCTCTCGTT CATCGGTATC ATTACCCCCA TGAACAGAAA TTCCCCCTTA
 AAGTCAATG GCCCGTACAA GTAGTAGTCA TTGGGCATAG CACTCGTAGG AGAGAGCAA GTAGCCATAG TAATGGGGGT ACTTGCTCTT AAGGGGAAT

 2801 CACGGAGGCA TCAAGTGACC AAACAGGAAA AAACCGCCCT TAACATGGCC CGCTTTATCA GAAGCCAGAC ATTAACGCTT CTGGAGAAAC TCAACGAGCT
 GTGCCCTCCGT AGTTCACCTG TTTGTCTCTT TTTGGCGGGA ATGTACCGG GCGAATAGT CTTCGGTCTG TAATGCGAA GACCTCTTTG AGTTGCTCGA

 2901 GGACGCGGAT GAACAGGCAG ACATCTCTGA ATCGCTTCAC GACCACGCTG ATGAGCTTTA CCGCAGGATC CGGAATGTGT AAACGTTAAT ATTTGTGTAA
 CCTGGCGCTA CTTGTCCGTC TGTAGACACT TAGCGAAGTG CTGGTGGCAG TACTCGAAT TACTCGAAT GCCTTTAACTA TTGCAATTA TAAACAATTT

 3001 AATTCGCGTT AAATTTTGT TAAATCAGCT CATTTTTTAA CCAATAGGCC GAAATCGGCA AAATCCCTTA TAAATCAAAA GAATAGACCG AGATAGGGTT
 TTAAGCGCAA TTTAAAAACA ATTTAGTCGA GTAAAAAAT GGTATCCGG CTTTAGCCGT TTTAGGGAAT ATTTAGTTTT CTTATCTGCG TCTATCCCAA

 3101 GAGTGTGTT CCAGTTTGA ACAAGAGTCC ACTATTAAAG AACGTGGACT CCAACGTCAA AGGGCGAAA ACCGTCTATC AGGGCTATGG CCCACTAGT
 CTCACAACAA GGTCAAACCT TGTCTCAGG TGATAATTC TTGCACCTGA GGTGACGTT TCCCGCTTTT TGGCAGATAG TCCCGATACC GGGTGATGCA

FIG. 32D

3201 GAACCAATCAC CCTAATCAAG TTTTTTTGGG TCGAGGTGCC GTAAAGCACT AAATCGGAAC CCTAAAGGGA GCGCCCGGATT TAGAGCTTGA CGGGGAAAGC
 CTTGGTACTG GGATTAGTTC AAAAAACCC AGCTCCACGG CATTTCTGTA TTAGACCTTG GGATTTCCCT CGGGGGCTAA ATCTCGAAT GCGCCCTTTCG

 3301 CGGCGAAGCT GCGGAGAAAG GAAGGGAAGA AAGCGAAGG AGCGGGCGCT AGGGCGCTGG CAAGTGTAGC GGTACAGCTG CGCGTAACCA CCACACCCCG
 GCGGCTTGCA CCGCTCTTTC CTTCCCTTCT TTTCCCTTCT TTTCCCTTCT TTTCCCTTCT TTTCCCTTCT TTTCCCTTCT TTTCCCTTCT TTTCCCTTCT

 3401 CGCGCTTAAT GCGCGGCTAC AGGCGGCTG CCGATCTGTC CTGCGCGCTT TCGGTGATGA CCGTGAAAC CTCTGACACA TGCAGCTCCC GGAGACGCTC
 GCGCGAATTA CGCGGCGATG TCCCGGCGAG GCCTAGGACG GAGCGGCGAA AGCCACTACT GCCACTTTTG GAGACTGTGT ACGTCGAGGG CCTCTGCCAG

 3501 ACAGCTTGTG TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGGCG GTCAGGGGGT GTTGGGGGGT GTCGGGGGCG AGCATGACC CAGTCACGTA
 TGTGGAACAG ACATTGCGCT ACGGCCCTCG TCTGTTCGGG CAGTCCCGCG CAGTCGCCCA CAACCGCCCA CAGCCCCGCG TCGGTACTGG GTCAGTGCAT

 3601 GCGATAGCGG AGTGTATACT GGCTTAAC TA TCGGGCATCA GAGCAGATTG TACTGAGAGT GCACCATATG CCGTGTGAAA TACCGCACAG ATGCGTAAGG
 CGCTATCGCC TCACATATGA CCGAATTGAT ACGCCGTAGT CTGCTCTAAC ATGACTCTCA CGTGTGTATAC GCCACACTTT ATGGCGGTGC TACGCATTC

 3701 AGAAATACC GCATCAGGG CTCTTCCGT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTTCCGGTGC GCGAGCGGT ATCAGCTCAC TCAAAGGCGG
 TCTTTTATGG CGTAGTCCG GAGAAGCGA AGGAGCGAGT GACTGAGCGA CCGAGGCCAG CAAGCCGACG CCGCTCGCCA TAGTCGAGTG AGTTTCCGCG

 3801 TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGCC CAGGAACCGT AAAAAGGCGG CGTTGCTGGC
 ATTATGCCAA TAGGTGTCTT AGTCCCTTAT TCGCTCTCTT CTGTGACTCT CTTTTTCCG TCGTTTTCCG GTCCTTGGCA TTTTTCCGCG GCAACGACCG

 3901 GTTTTTCCAT AGGCTCCGCG CCCTGACGA GCATCACA AAATCGACGT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA CCAGGCGTTT
 CAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTCTTT TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGTGTCTTG ATATTCTAT GGTCCGCAAA

 4001 CCCCCTGGAA GCTCCCTCTGT GCGCTCTCTT GTTCCGACCC TGCCGCTTAC CCGATACCTG TCCGCTTTC TCCCTTCCG AAGCGTGGG CTTTCTCATA
 GGGGGACCTT CGAGGGAGCA CCGGAGAGA CAAGCTGGG ACGGCGAATG GCCTATGGAC AGGCGGAAAG AGGGAAGCCC TTTCGACCCG GAAAGAGTAT

 4101 GCTCAGCGTG TAGGTATCTC AGTTCCGGTG AGTTCGGTTC CTCCAGCTG GCGTGTGTGC ACGAACCCCG CGTTCAGCCC GACCGCTGCG CCTATATCCG
 CGAGTGGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC GAGGTCTGAC CCGACACAG TGCTTGGGG GCAAGTCCGG CTGGCGACCG GGAATAGGCC

 4201 TAACTATCGT CTTGATCTCA ACCCGGTAAG ACACGACTTA TCGGCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGCGGGTGCT
 ATTGATAGCA GAATCAGGT TGGGCCATTC TGTGCTGAAT AGCGTGACC GTCTCGGTG ACCATTGTCC TAATCGTCTC GCTCCATACA TCCGCCACGA

FIG. 3a

4301 ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA GAAGGACAGT ATTGTGGTATC TGGCGTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG
 TGTCTCAAGA ACTTCACAC CCGATTGAT CCGATTGAT CTTCTGTGCA TAAACCATAG ACGGAGAGC ACTTCGGTCA ATGGAAGCCT TTTTCTCAAC
 4401 GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC
 CATCGAGAAC TAGGCGGTTT GTTTGGTGGC GACCATCGCC ACCAAAAAAA CAAACGTCG TCGTCTAATG CCGGTCITTT TTTCTCTAGG TTCTTCTAGG
 4501 TTTGATCTTT TCTACGGGT CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGATTTT GGTCAATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCCT
 AAAC TAGAAA AGATGCCCCA GACTGCGAGT CACCTTGCTT TTGAGTGCAA TTCCCTAAAA CCAGTACTCT AATAGTTTTT CCTAGAAGTG GATCTAGGAA
 4601 TTAATATAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT GCTTAATCAG TGAGGCACCT ATCTCAGCGA
 AATTATAATT TTACTTCAAA ATTTAGTTAG ATTTCAATATA TACTCATTTG AACAGACTG TCAATGGTTA CGAATTAGTC ACTCCGTGGA TAGAGTCGCT
 4701 TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCGT GCTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGTG CAATGATACC
 AGACAGATAA AGCAAGTAGG TATCAACGGA CTGAGGGGCA GCACATCTAT TGATGCTATG CCTCCCGAA TGCTAGACCG GGTTCACGAC GTTACTATGG
 4801 GCGAGACCCA CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCTCG CAACTTTATC CGCTTCATC
 CGCTCTGGGT GCGAGTGGCC GAGGTCTAAA TAGTCTGTTAT TTGGTCTGCT GGCCTTCCCG GCTCGGCTCT TCACCAGGAC GTTGAATAAG GCGGAGGTAG
 4901 CAGTCTATTA ATTGTTGCGG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA TAGTTTGGC AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT
 GTCAGATAAT TAACAACGGC CCTTCGATCT CATTCATCAA CGGCTCAATT ATCAAAACCG TTGCAACAAC GGTAAACGACG TCCGTAGCAC CACAGTGCGA
 5001 CGTCTGTTGG TATGGCTTCA TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCT CTTCTGGTCC
 GCAGCAAACC ATACCGAAGT AAGTCGAGGC CAAGGGTTGC TAGTTCCGCT CAATGTACTA GGGGGTACAA CACGTTTTTT CGCCAATCGA GGAAGCCAGG
 5101 TCCGATCGTT GTCAGAAATA AGTTGGCCGC AGTGTTATCA CTCATGGTTA TGGCAGCACT GCATTAATCT CTTACTGTCA TGCCATCCGT AAGATGCTTT
 AGGCTAGCAA CAGTCTTCAT TCAACCGGCG TCACAATAGT GAGTACCAAT ACCGTCGTGA CGTATTAGA GAATGACAGT ACGGTAGGCA TTCTACGAAA
 5201 TCTGTGACTG GTGAGTACTC AACCAGTCA TTCTGAGAAAT AGTGATGCG GCGACCGAGT TGTCTTGGC CGGGGTCAAC ACGGATAAT ACCGCGCCAC
 AGACACTGAC CACTCATGAG TTGGTTCACT AAGACTCTTA TCACATACGC CGCTGGCTCA ACGAGAACGG GCCGAGTTG TGCCCTATTA TGGCGCGGTG

FIG. 32F

5301 ATAGCAGAAC TTATAAAGTG CTCATCAATG GAAAACGTTT TCGGGGGCGA AAAGTCTCAA GGAFTTACC GCTGTTGAGA TCCAGTTTCA TGTAACCCAC
 TATCGTCTTG AAATTTTCAC GAGTAGTAAC CTTTGTCAAG AAGCCCCGCT TTTGAGAGTT CCTAGAATGG CGACAATCT AGGTCAAGCT ACATTGGGTG
 5401 TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC AGCGTTTCTG GGTGAGCAAA AACAGGAAGG CAAAAAGCG CAAAAAGGG AATAAGGGCG
 AGCACGTGGG TTGACTAGAA GTCGTAGAAA ATGAAAGTGG TCGCAAGAC CCACTCGTTT TTGTCCTTCC GTTTTACGGC GTTTTTCCTC TTATTCCCCG
 5501 ACACGGAAAT GTTGAATACT CATACTCTTC CTTTTTCAAT ATTATTGAAG CATTTATCAG GGTATTGTC TCATGAGCGG ATACATATTT GAATGTATTT
 TGTGCCCTTA CAACCTATGA GTATGAGAAG GAAAAAGTAA TAATAACTTC GTAAATAGTC CCAATAACAG AGTACTCGCC TATGTATAAA CTTACATAAA
 5601 AGAAAAATAA ACAATAGGG GTTCCGGCGA CATTTCCCGG AAAAGTGCCA CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG
 TCTTTTTTATT TGTATTATCC TGTTTATCCC CAAGGCGCGT GTAAAGGGGC TTTTACCGGT GGAATGAGA TTTCTTGGTA ATAAATAGTAC TGTAAATGGA TATTTTTATC
 5701 GCGTATCAG AGGCCCTTTC GTCTTCAATA CAGGTAGACC TTTTCGTAGAG ATGTACAGTG AAATCCCGA AATTATACAC ATGACTGAAG GAAGGGAGCT
 CGCATAGTGC TCCGGGAAAG CAGAAGTTAT GTCCATCTGG AAAGCATCTC TACATGTAC TTTAGGGGCT TTAATATGTG TACTGACTTC CTTCCCTCGA
 5801 CGTCATTCCC TCGCGGGTTA CGTCACCTAA CATCACTGTT ACTTTAAAAA AGTTTCCACT TGACACTTTG ATCCCTGATG GAAAACGCAT AATCTGGGAC
 GCAGTAAGGG ACGGCCCAAT GCAGTGGATT GTAGTGACAA TGAAATTTTT TCAAAGGTGA ACTGTGAAAC TAGGGACTAC CTTTTCGGTA TTAGACCTG
 5901 AGTAGAAAGG GCTTCATCAT ATCAAATGCA ACGTACAAAG AAATAGGCT TCTGACCTGT GAAGCAACAG TCAATGGGCA TTTGTATAAG ACAAACTATC
 TCATCTTTCC CGAAGTAGTA TAGTTTACGT TGTATCCCGA AGACTGGACA CTTTCTGTC AGTTACCCGT AAACATATTC TGTGTGATAG
 6001 TCACACATCG ACAAAACCAAT ACAATACAGG TAGACCTTTC GTAGAGATGT ACAGTGAAT CCCCAGAAAT ATACACATGA CTGAAGGAAG GGAGCTCGTC
 AGTGTGTAGC TGTGTTGTTA TGTATGTCC ATCTGGAAAG CATCTCTACA TGTCACTTTA GGGGCTTTAA TATGTGTACT GACTTCTTTC CCTCGAGCAG
 6101 ATTCCCTGCC GGGTTAGTCC ACCTAACATC ACTGTTACTT TAAAAAGTT TCCACCTGAC ACTTTGATCC CTGATGGAAA ACGCATATC TGGGACAGTA
 TAAGGGACGG CCCAATGCAG TGGATTGTAG TGACAATGAA ATTTTTTCAA AGGTGACTG TGAACCTAGG GACTACCTTT TCGGTATTAG ACCCTGTCTAT
 6201 GAAAGGGCTT CATCATATCA AATGCAACGT ACAAGAAAT AGGCTTCTG ACCCTGGAAG CAACAGTCAA TGGGCATTTG TATAAGACAA ACTATCTCAC
 CTTTCCCGAA GTAGTATAGT TTACGTTGCA TGTCTCTTTA TCCCGAAGAC TGGACACTTC GTTGTCAAGT ACCCGTAAAC ATATTCTGTT TGATAGAGTG
 6301 ACATCGACAA ACCAATACAA TCTACAGGTA GACCTTTCGT AGAGATGTAC AGTGAATCC CCGAAATAT ACACATGACT GAAGGAAGGG AGCTCGTCTAT
 TGTAGCTGTT TGGTTATGTT AGATGTCCAT CTGGAAGCA TCTCTACATG TCACTTTAGG GGCCTTAATA TGTGTACTGA CTTCTCTTCC TCGAGCAGTA
 6401 TCCCTGCCGG GTTACGTCAC CTAACATCAC TGTACTTTA AAAAGTTTC CACTTGACAC TTTGATCCCT GATGGAAGC GCATAATCTG GGACAGTAGA
 AGGGACGGCC CAATGCAGTG GATTGTAGTG ACAATGAAAT TTTTTCAAAG GTGAACGTGT AACTTAGGGA CTACCTTTTG CGTATTAGAC CCTGTCTCT
 6501 AAGGGCTTCA TCATATCAAA TGCAAGGTAC AAAGAAATAG GGCTTCTGAC CTGTGAAGCA ACAGTCAATG GGCATTTGTA TAAGACAAAC TATCTCACAC
 TTCCCGAAGT AGTATAGTTT ACGTTGCATG TTTCTTTTAT CCGAAGACTG GACACTTCTG TGTCAAGTAC CCGTAAACAT ATTCTGTGTTG ATAGAGTGTG
 6601 ATCGACAAAC CAATACAATC
 TAGCTGTTTG GTTATGTTAG

FIG. 326

1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGTTATTAAAT TACGGGGTCA TTAGTTTATA GCCCATATAT GGAGTCCGC GTTACATAAC
AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCAATAATTA TCATTAGTTA ATGCCCCAGT AATCAAGTAT CCGGTATATA CCTCAAGGCG CAATGTATTG
101 TTACGGTAAA TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGAATTCCCA
AATGCCATTT ACCGGGCGGA CCGACTGGCG GGTGCTGGG GGGGGGTAAC TGCAGTTATT ACTGCATACA AGGTATCAT TCGGTTATC OCTGAAAGGT
201 TTGACGTCAA TGGGTGGAGT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGA TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT
AACTGCAGTT ACCCACCCTCA TAAATGCCAT TTGACGGGTG AACCGTCATG TAGTTCACAT AGTATACGGT TCATGCGGGG GATAACTGCA GTTACTGCCA
301 AAATGGCCCG CCTGGCATTA TGCCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC
TTTACCGGGC GGACCGTAAT ACGGTCATG TACTGGAATA CCTGAAAGG ATGAACCGTC ATGTAGATGC ATAAATCAGTA GCGATAATGG TACCACCTAGC
401 GGTTTTGGCA GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC TCCACCCCAT TGACGTCAT GGGAGTTTGT TTTGGCACCA
CCAAAACCGT CATGTAGTTA CCCGCACCTA TCGCCAAACT GAGTGCCCCCT AAAGTTTACG AGTGGGGTA ACTGCAGTTA CCTCAACA AAACCGTGCT
501 AAATCAACGG GACTTTCCAA AATGTCGTAA CAACTCGCC CCATTGACG AATGGGCGG TAGGCGTGA CCGTGGGAGG TCTATATAAG CAGAGCTCGT
TTTAGTTGCC CTGAAAGGTT TTACAGCATT GTTGAGCGG GGTAACTGG TTTACCCGCC ATCCGCACAT GGCACCCCTCC AGATATATTC GTCTCGAGCA
601 TTAGTGAACC GTCAGATCGC CTGGAGACGC CATCCACGCT GTTTTGACCT CCATAGAAGA CACCGGGACC GATCCAGCCT CCGCGGCCCG GAACGGTGCA
AATCACTGG CAGTCTAGCG GACCTCTGG GTAGGTGCGA CAAAACCTGA GGTATCTTCT GTGGCCCTGG CTAGGTCCGA GCGCGCCGCC CTTGCCACGT
701 TTGGAACGG GATTCGCCGT GCCAAGAGTG ACGTAAGTAC CGCCTATAGA GTCTATAGG CACCCCCCTT GGCTTCGTTA GAACGCGGCT ACAATTAATA
AACCTTGCGC CTAAGGGGCA CCGTTCTCAC TGCATTATG CCGGATATCT CAGATAATCC GGTGGGGGAA CCGAAGCAAT CTTGCGCCGA TGTAAATAT
801 CATAACCTTA TGTATCATAC ACATACGATT TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT CCACTCCCG GTCCAACCTGC
GTATTGGAAT ACATAGTATG TGTATGCTAA ATCCACTGTG ATATCTTATT GTAGTGAAA CGGAAAGAGA GGTGTCCACA GGTGAGGTC CAGGTTGACG
901 ACCTCGGTC TATCGATTGA ATTCCACCAT GGGATGGTCA TGTATCATCC TTTTCTTAGT AGCAACTGCA ACTGGAGTAC ATTCAGATAT CCAGATGACC
TGGAGCCAAG ATAGCTAACT TAAGGTGCTA CCTTACCAGT ACATAGTAGG AAAAAGATCA TCGTTGACGT TGACCTCATG TAAGTCTATA GGTCTACTGG
1 M G W S C I I L F L V A T A T G V H S D I Q M T
^met ^Start VL ^EcoRV

FIG. 33 A

1001 CAGTCCCCGA GTCCTCTGTG CGCCTCTGTC GCCTATGAGG TCACCATCAC CTGCGTGCC AGTCAGGATG TGTCCACTTC TGTAGCCTGG TATCAACAGA
 GTCAGGGGCT CGAGGGACAG CGGAGACAC CCGCTATCCC AGTGGTAGTG GACGGACGG TCAGTCTTAC ACAGGTGAGG ACATCGGACC ATAGTTGTCT
 25 Q S P S S L S A S V G D R V T I T C R A S Q D V S T A V A W Y Q Q K
 ^CDR-L1
 1101 AACCAGGAAA AGCTCCGAAG CTTCTGATTT ACTCGGCATC CTTCTCTTAC TGTGGAGTCC CTTCTCGCTT CTCCTGTAGC GGTTCGGGA CGGATTTTCAC
 TTGGTCCCTTT TCGAGGGCTTC GAAGACTAAA TGAGCCGTTAG GAAGAGATG AGACCTCAGG GAAGACGAA GAGACCATCG CCAAGGCCCT GCCTAAAGTG
 59 P G K A P K A P K L L I Y S A S F L Y S G V P S R F S G S G S G T D F T
 ^CDR-L2
 1201 TCTGACCATC AGCAGTCTGC AGCCGGAAGA CTTCCGCAACT TATTACTGTC AGCAATCTTA TACTACTCCT CCACGTTTCG GACAGGTAC CAAGGTGGAG
 AGACTGGTAG TCGTCAGACG TCGGCCCTTCT GAAGCCTTGA ATAATGACAG TCGTTAGAAT ATGATGAGGA GGGTGCAAGC CTGTCCCATG GTTCCACCTC
 92 L T I S S L Q P E D F A T Y Y C Q Q S Y T T P P T F G Q G T K V E
 ^CDR-L3
 1301 ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCACTCTCC CGCCATCTGA TGAGCAGTTG AAATCTGGAA CTGCTTCTGT TGTGTGCCCTG CTGAATAACT
 TAGTTTGCTT GACACCGAGG TGGTAGACAG AAGTGAAGG GCGGTAGACT ACTCGTCAAC TTTAGACCTT GACGAAGACA ACACACGGAC GACTTATTGA
 125 I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L N N F
 ^start human kappa
 401 TCTATCCCAG AGAGGCAAA GTACAGTGA AGGTGGATA CGCCTCCAA TCGGGTAACT CCCAGGAGAG TGTACACAG CAGGACAGCA AGGACAGCAC
 AGATAGGGTC TCTCCGGTTT CATGTCACCT TCCACCTATT GCGGAGGTT AGCCCATTTA GGTCTCTTC ACAGTGTCTC GTCCTGTCTG TCCTGTCTGT
 159 Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T
 501 CTACAGCCTC AGCAGCACCC TGACGCTGAG CAAAGCAGAC TAGGAGAAAC ACAAGTCTA CGCCTGGGAA GTCACCCATC AGGGCCTGAG CTCGCCCGTC
 GATGTCGGAG TCGTCGTGG ACTGCGACTC GTTTCGCTCG ATGCTCTTTG TGTTCAGAT GCGGACGCTT CAGTGGGTAG TCCCGGACTC GAGCGGGCAG
 192 Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V
 601 ACAAGAGCT TCAACAGGGG AGAGTGTAA GCTTGGCCGC CATGGCCCAA CTGTGTTATT GCAGTTATA ATGTTTACAA ATAAAGCAAT AGCATCACAA
 TGTGTTCTGA AGTTGTCCCC TCTCACAATT CGAACCGGG GTACCGGGT GAACAAATAA CGTCAATAT TACCAATGTT TATTTCGTTA TCGTAGTGTT
 225 T K S F N R G E C O

FIG. 33b

1701 ATTTCACAAA TAAAGCAATT TTTTCACTGC ATTCTAGTTG TGGTTTGTCC AAACATCATCA ATGTATCTTA TCATGTCTGG ATCGGGAATT AATTCCGGCGC
 TAAAGTGTTT ATTTCGTTAA AAAAGTGACG TAAGATCAAC ACCAAACAGG TTTTGAGTAGT TACATAGAAT AGTACAGACC TAGCCCTTAA TTAAAGCCGCG
 1801 AGCACCATGG CCTGAAATAA CCTCTGAAAG AGGAACCTGG TTAGGTATCT TCTGAGGGGG AAAGAACCAG CTGTGGAATG TGTGTCAATT AGGGTGTGGA
 TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATAGA AGACTCCGCC TTTCTTGGTC GACACCTTAC ACACAGTCAA TCCCACACCT
 ^change from C to T, kill KpnI site
 1901 AAGTCCCCAG GCTCCCCAGC AGGCAGAAAT ATGCAAGCA TGCATCTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC AGGTCCCCA GCAGGCAGAA
 TTCAGGGGTC CGAGGGGTCG TCCGTCCTCA TACGTTTCGT ACCTAGAGTT AATCAGTCGT TGGTCCACAC CTTTCAGGGG TCCGAGGSET CGTCCGTCIT
 2001 GTATGCAAAG CATGCATCTC AATTAGTCAG CAACCATAGT CCGCCCCCTA ACTCCGCCCA TCCCGGCCCT AACTCCGCC AGTTCGCC ATTCGCCGCC
 CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGGTATCA GGGCGGGGT TGAGCGGGG TTAGAGCGGG TCAAGGCGGG TAAGAGGCGG
 2101 CCATGGCTGA CTAATTTTTT TTATTTATGC AGAGGCCGAG GCGCCCTCG CCTCTGAGCT ATTCAGAAAG TAGTGAGGAG GCTTTTTTGG AGCCCTAGGC
 GGTACCGACT GATTAAAAA AATAAATAGG TCTCCGGCTC GGGCGGAGCC GGAGACTCGA TAAGTCTTTC ATCCTCTC CGAAAAAAC TCCGGATCCG
 2201 TTTTGC AAAA AGCTGTTAAC AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTACTGGG AAAACCTCG CGTAPACCAA CTTAATCGCC TTGCAGCACA
 AAAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AAATGTTGCA GCACTGACCC TTTTGGGACC GCAATGGGT GAATTAGCGG AACGTCTGT
 2301 TCCCCCCTTC GCCAGCTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCCTAGC CTGAATGGCG AATGGCGCCT GATGCCGTAT
 AGGGGGGAAG CCGTCGACCG CATTATCGCT TCTCCGGGCG TGGCTAGCG GAAGGTTGT CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA
 2401 TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAC GTCAAAGCAA CCATAGTACG CGCCTGTAG CGCGCATTA AGCGCGCGG GTGTGTGTGT
 AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGGCTATG CAGTTTCTGT GGTATCATGC GCGGACATC GCCCGGTAAT TCGCGCGGCC CACACACCA
 2501 TACGGCAGC GTGACCGCTA CACTTGCCAG CGCCCTAGCG CCGCTCTCTT TCGCTTCTCT CCCTTCTCTT CTCGCCACGT TCGCCGGCTT TCCCGGTCAA
 ATGCGCGTCG CACTGGCGAT GTGAACGGTC GCGGATCGC GGGCAGGAA AGCGAAGAA GGAAGGAA GAGCGGTGCA AGCGCGCGA AGGGCAGTT
 2601 GCTCTAATC GGGGGCTCCC TTTAGGGTTC CGATTATAGT CTTTACGGCA CCTCGACCCC AAAAACTTG ATTTGGGGA TGGTTCACGT AGTGGGCCAT
 CGAGATTAG CCCCCGAGG AATCCCAAG GCTAAATCAC GAAATGCCGT GGAGCTGGG TTTTGTGAAC TAAACCCACT ACCAAGTGCA TCACCCGGTA

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FIG. 33 C

2701 CGCCCTGATA GACGGTTTTT CGCCCTTTGA CGTTGGAGTC CACGTTCTTT AATAGTGGAC TCTTGTTC AACTGGAACA AACTCAACC CTATCTCGG
 GCGGACTAT CTGCCAAAA GCGGAACT GCAACCTCAG GCAACCTCAG GTGCAAGAAA TTATCACCTG AGAACAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC
 2801 CTATTCTTTT GATTATTAAG GGATTTTGGC GATTTCGGCC TATTGTTAA AAAATGAGCT GATTTAACA AAAATTTAACG CGAATTTTAA CAAAATATTA
 GATAAGAAAA CTAAATATTC CTTAAACCG CTAAAGCCGG ATAACCAATT TTTTACTCGA CTAAATTGTT TTTAAATTGC GCTTAAATTT GTTTTATAAT
 2901 ACGTTTACAA TTTTATGTTG CACTCTCAGT ACAATCTGCT CTGATGCCG ATAGTTAAGC CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGCGCC
 TGCAAATGTT AAAATACCAC GTGAGAGTCA TGTAGACGA GACTACGGCG TATCAATTCC GTTGAGGCGA TAGCGATGCA CTGACCCAGT ACCGACGCGG
 3001 CCGACACCCG CCAACACCCG CTGACGGGCT TGTCTGCTCC CGGCATCCGC TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT
 GGCTGTGGG GGTGTGGG GACTGCGCG GACTGCCCGA ACAGACGAGG GCGTAGGCG AATGCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA
 3101 CAGAGGTTT CACCGTCATC ACCGAAACGC GCGAGGCAGT ATTCTTGAAG ACGAAAGGC CTCGTGATAC GCTTATTTT ATAGTTTAAAT GTCATGATAA
 GTCTCCAAA GTGGCAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACTTC TGTCTCCG GAGCACTATG CGGATAAAA TATCCAATTA CAGTACTATT
 3201 TAATGGTTT TTAGACGTCA GGTGGCACTT TTCGGGAAA TGTGGCGGA ACCCTATTT GTTATTTTT CTAAATACAT TCAAAATATGT ATCCGCTCAT
 ATTACCAAAG AATCTGCAGT CCACCGTGAA AAGCCCCCTT ACACGGCCT TGGGGATAAA CAAATAAAA GATTTATGTA AGTTTATACA TAGGCGAGTA
 3301 GAGACAAATA CCTGATAA TGCTTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT TCGCGCATTT
 CTCGTGTATT GGGACTATTT ACGAAGTTAT TATTAATTTT TCCTTCTCAT ACTCATAGT TGTAAGGCA CAGCGGGAAT AAGGAAAAA ACGCGTAAA
 3401 TGCCTTCTG TTTTGTCTCA CCCAGAACG CTGTTGAAAG TAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA
 ACGGAAGGAC AAAAACGAGT GGGTCTTTGC GACCACCTTC ATTTTCTACG ACTTCTAGTC AACCCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT
 3501 GCGGTAAGAT CCTTGAGAT TTTTCGCCCG AAGAAGTTT TCCAATGATG AGCATTTTA AGTTCTGCT ATGTGGCGG GTATTATCCC GTGATGACGC
 CGCCATTCTA GGAACCTCA AAAGCGGGC TTCTTGCAA AGGTTACTAC TCGTGAAAAT TTCAAGACGA TACACCGCGC CATAATAGG CACTACTGCG
 3601 GGGGAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTGG TTGAGTACTC ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA
 GCGCGTTCTC GTTGAGCCAG CCGCGTATGT GATAAGATC TTAAGAACC AACTCATGAG TGGTCAGTGT CTTTTCTGAG AATGCTTACC GTACTGTCTAT

57/75

FIG. 33 D

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3701 AGAGATTAT GCAGTGCTGC CATAACCATG AGTGATPACA CTGGGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACG GCCTTTTTCG
    TCCTCTTAATA CGTCACGACG GTATTGGTAC TCACATATGT GACGCCGCTT GAATGAAGAC TGTGTCTAGC CTCCTGGCTT CCTCGATGG CGAAAAAAGC

3801 ACACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAAACGA CGAGCGTGAC ACCACGATGC CAGCAGCAAT
    TGTGTATACC CCTAGTACAT TGAGCGGAAC TAGCAACCCCT TGGCCTCGAC TTACTTCGCT ATGTTTGCT GCTCGCACTG TGGTGTCTAG GTCTCGTTA

3901 GGCAACAACG TTGGCGCAAC TATTAACTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC TGGATGGAG CGGATAAAGT TGCAGGACCA
    CCGTTGTTGC AACGCTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCCTTGT TAATTATCTG ACCTACCTCC GCCTATTICA ACCTCCTGGT

4001 CTCTCTGGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG GGGCCAGATG
    GAAGACGCGA GCGGGAAG CCGACCGACC AAATAACGAC TATTTAGACC TCGGCCACTC GCACCAGAG CGCCATAGTA ACGTCTGTAC CCCGGTCTAC

4101 GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC GAAATAGACA GATCGGTGAG ATAGGTGCTT CACTGATTAA
    CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCTC AGTCCGTTGA TACCTACTTG CTTTATCTGT CTAGGACTC TATCCACGGA GTGACTAATT

4201 GCATTGGTAA CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAACCTTCA TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCCTTTTGAT
    CGTAACCAAT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAATAA ATTTTGAAGT AAAAATTA TTTTCTAGA TCCACTTCTA GGAATAACTA

4301 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTCTC ACTGAGGCTC AGACCCCGTA GAAAGATCA AAGGATCTTCTT TTTTCTTCTG
    TTAGAGTACT GGTTTTAGG AATTGCACCT AAAAGCAAG TGACTCGCAG TCTGGGGCAT CTTTCTAGT TTCCTAGA AACTCTAGGA AAAAAAGAGC

4401 GCGTAATCTG CTGCTTGCAA AAAAAAAC CACCGCTACC AGCGGTGGTT TGTTCGCGG ATCAAGAGCT ACCAATCTT TTTCGGAAG TAACTGGCTT
    CGCATTAGAC GACGAACGTT TGTTTTTTTG GTGGCGATGG TCGCCACCAA ACAACCGCC TAGTTCTGTA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA

4501 CAGCAGAGCG CAGATACCAA ATACTGTCTT TCTAGTGTAG CCGTAGTAG GCCACCACTT CAAGAATCTT GTAGCACCGC CTACATACCT CGCTCTGCTA
    GTCGTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CGGTGTGAA GTTCTTGAGA CATCTGGCG GATGTATGGA GCGAGACGAT

4601 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCTG GTCTTACCG GTTGGACTCA AGAGGATAGT TACCGATAA GCGCGACGG TCGGGCTGAA
    TAGGACAAATG GTCACCGAGC ACGCTACCG CTATTTCAGA CAGAATGGCC CAACCTGAGT TCTGCTATCA ATGGCTTATT CCGGCTGCGC AGCCCGACTT

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4701 CCGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCCGAAGG
 GCGCCCCAAG CACGTGTGTC GGGTCGAACC TCGCTTGCTG GATGTGGCTT GACTCTATGG ATGTCGCACT CGTAACTCTT TCGCGGTGCG AAGGGCTTCC

 4801 GAGAAAGCG GACAGGTATC CGGTAAGCG CAGGGTCGGA ACAGGAGAGC GCACGAGGA GCTTCCAGGG GGAACGCCCT GGTATCTTTA TAGTCTGTG
 CTCCTTCCGC CTGTCCATAG GCCATTCCGC GTCCCAGCCT TGTCTCTCG CGTGCTCCT CGAAGGTCCC CTTTGGCGA CCATAGAAAT ATCAGGACAG

 4901 GGGTTTCGCC ACCCTGACT TGAGCGTGA TTTTGTGAT GCTGCTCAG GGGCGGAGC CTATGGAAA ACGCCAGAA CGCGGCCCTT TTACGGTTCC
 CCCAAGCGG TGGAGACTGA ACTCGCAGCT AAAAACACTA CGAGCAGTCC CCCGCTCG GATACCTTTT TCGGTCGTT GCGCCGAAA AATGCCAAGG

 5001 TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTCTCTGC GTTATCCCCT GATCTGTGG ATAACCGTAT TACCGCCCTT GAGTGAGCTG ATACCGCTCG
 ACCGGAAAAC GACCGGAAA CGAGTGTACA AGAAGGACG CAATAGGGA CTAAGACACC TATTGGCATA ATGGCGGAAA CTCACCTCGAC TATGGCGAGC

 5101 CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCG CGCGTTGGCC GATTCATTAA
 GCGCTCGGCT TGCTGGCTCG CGTGGCTCAG TCACCTCGCTC CTTCGCCCTT TCGCGGTTA TCGGTTGGC GGAGAGGGGC GCGCAACCG CTAAGTAATT

 5201 TCCAGTGGC ACGACAGGT TCCCGACTGG AAAGCGGCA GTGAGCGCA CGCAATTAA GTGAGTTACC TCACCTCATTA GGCACCCAG GCTTTTACACT
 AGGTGACCG TGCTGTCCA AAGGCTGACC TTTCGCCCCG CACTCGCGTT GCGTTAATTA CACTCAATGG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA

 5301 TTATGCTTCC GGCTCGTATG TTGTGTGGA TTGTGAGCGG ATAAACAATT CACACAGGA ACAGCTATGA CCATGATTAC GAATTAA
 AATACGAAG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTAAA GTGTGTCTT TGTGATACT GGTACTAATG CTTAATT

FIG. - 33 F

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1  ATTCCGAGCTC GCCCGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTTCAT AGCCCATATA TGGAGTTCCG CGTTACATAA
   TAAGCTCGAG CGGGCTGTAA CTAATAACTG ATCAATAATT ATCAATTAGTT AATGCCOCAG TAATCAAGTA TCGGGTATAT ACCTCAAGGC GCAATGTATT

101 CTTACGGTAA ATGGCCGCC TGGCTGACCG CCCAAGACC CCCGCCCATT GACGTCAATA ATGACGATAG TTCCCATAGT AACGCCAATA GGGACTTTCC
   GAATGCCATT TACCGGGCGG ACCGACTGGC GGGTTGCTGG GGGGGGTAA CTGCAGTTAT TACTGCATAC AAGGGTATCA TTGCGGTTAT CCTGAAAGG

201 ATTGACGTCA ATGGGTGGAG TATTACGCT AAACTGCCCA CTGGCCAGTA CATCAAGTGT ATCAPATGCC AAGTACGGCC CCTATTGACG TCAATGACGG
   TAACTGCAGT TACCCACCTC ATAAATGCCA TTTGACGGGT GAACCGTCAAT GTAGTTCACA TAGTATACGG TTCAATGCGGG GGATAACTGC AGTTACTGCC

301 TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA TCGCTATTAC CATGGTGATG
   ATTTACCGGG CGGACCGTAA TACGGGTCAAT GTACTGGAAAT ACCCTGAAAG GATGAACCGT CATGTAGATG CATTAATCAGT AGCGATAATG GTACCCACTAC

401 CGGTTTGGC AGTACATCAA TGGGCGTGGG TAGCGGTTTG ACTACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA TGGGAGTTTG TTTTGGCACC
   GCCAAAACCG TCATGTAGTT ACCCGCACCT ATCGCCAAAC TGAGTGCCCC TAAAGTTCA GAGGTGGGGT AACTGCAGTT ACCCTCAAAC AAAACCGTGG

501 AAAATCAACG GGACTTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGAGG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG
   TTTTACTTGC CCTGAAAGGT TTTACAGCAT TGTTCAGGCG GGGTAACATGC GTTTACCCGC CATCCGCACA TGCACCCCTC CAGATATATT CGTCTCGAGG

601 TTTAGTGAAC CGTCAGATCG CCTGGAGAGC CCATCCACGC TGTTTTGACC TCCATAGAG ACACCGGGAC CGATCCAGCC TCCGGCGGCG GGAACGGTGC
   AAATCACTTG GCAGTCTAGC GGACCTCTGC GGTAGGTGCG ACAAACCTGG AGGTATCTTC TGTGGCCCTG GCTAGGTGCG AGGCGCCGCG CCTTGCCACG

701 ATTGGAACGC GGATTCCCCG TGCCAAGAGT GACGTAAGTA CCGCTATAG AGTCTATAGG CCCACCCCTT TGGCTTCGTT AGAACGCGGC TACAATTAAT
   TAACCTTGC CTTAAGGGC ACGGTTCTCA CTGCATTTCAT GCGGATATC TCAGATATCC GGGTGGGGA ACCGAAGCAA TCTTGGCGCG ATGTTAATTA

801 ACATAACCTT ATGTATCATA CACATACGAT TTAGGTGACA CTATAGAATA ACATCCACTT TGCTTTCTC TCCACAGTG TCCACTCCA GGTCCAAC TG
   TGTATTGGAA TACATAGTAT GTGTATGCTA AATCCACTGT GATATCTTAT TGTAGGTGAA ACGGAAGAG AGGTGTCAC AGGTGAGGT CCAGGTTGAC

901 CACCTCGGTT CTATCGATTG AATTCCACCA TGGGATGGTC ATGTATCATC CTTTCTTAG TAGCAACTGC AACTGGAGCG TACGCTGAGG TTCAGCTGGT
   GTGGAGCCAA GATAGCTAAC TTAAGGTGGT ACCCTACCA G TACATAGTAG GAAAAAGATC ATCGTTGACG TTGACCTCGC ATGCGACTCC AAGTCGACCA
   1      M G W S C I I L F L V A T A T G A Y A E V Q L V
           ^start signal peptide
           ^met
           ^start of heavy chain
           ^BsiWI

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FIG. 34A

1001 GGAGTCTGGC GGTGGCCTGG TGCAGCCAGG GGGTCACTC CGTTTGTCCT GTGCAGCTTC TGGCTTCACC ATTAGTGGTT CTGGGATACA CTGGGTGCGT
 CCTCAGACCG CCACCGGACC ACGTCGGTCC CCCGAGTGAG GCAAACAGGA CACGTGCAAG ACCGAAGTGG TAATCACCAA GAACCTATGT GACCCACGCA
 25 E S G G G L V Q P G G S L R L S C A A S G F T I S G S W I H W V R
 ^CDR-H1
 1101 CAGGCCCCGG GTAAGGGCCT GGAATGGGTT GCTTGGATTG CTCCTTAATAG CGGGCTACT GACTATGCCG ATAGCGTCAA GGGCCGTTTC ACTATAAGCG
 GTCCGGGGCC CATTCGCCGA CATTCCCGGA CATTACCCAA CGAACCTAAC GAGGAATATC GCCCGGATGA CTGATACGGC TATCGCAGTT CCGGCAAG TGAATTCGC
 58 Q A P G K G L E W V A W I A P Y S G A T D Y A D S V K G R F T I S A
 ^CDR-H2
 1201 CAGACACATC CAAAAACACA GCCTACCTAC AATGAACAG CTTAAGAGCT GAGGACACTG CCGTCTATTA TTGTGCAAGA GAGGGGGGCT TGTACTGGGT
 GTCTGTGTAG GTTTTGTGT CCGATGGATG TTACTTGTG GAATCTCGA CTCCTGTGAC GGCAGATAAT AACACGTTCT CTCCTCCCGA ACATGACCCA
 92 D T S K N T A Y L Q M N S L R A E D T A V Y Y C A R E G G L Y W V
 ^CDR-H3
 1301 GTTCGACTAC TGGGGTCAAG GAACCCCTGGT CACCGTCTCC TCGGCTCCA CCAAGGGGCC ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT
 CAAGCTGATG ACCCCAGTTC CTTGGGACCA GTGGCAGAGG AGCCGAGGT GGTTCGCGG TAGCCAGAAG GGGGACCGTG GGAGGAGGTT CTGCTGGAGA
 125 F D Y W G Q G T L V T V S S A S T K G P S V F P L A P S S K S T S
 ^Apal
 1401 GGGGGCACAG CGGCCCTGGG CTGCCCTGTC AAGGACTACT TCCCGGAACC GGTGACGGTG TCGTGGAACT CAGGGCCCCCT GACCAGCGGC GTGCACACCT
 CCCCCGTGTC GCCGGGACCC GACGGACCCAG TTCCTGATGA AGGGCTTGG CCACGTGCCAC AGCACCTTGA GTCCGCGGGA CTGGTCGCCG CACGTGTGGA
 158 G G T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F
 1501 TCCCCGGCTGT CTTACAGTCC TCAGGACTCT ACTCCCTCAG CAGGTGGTG ACTGTGCCCT CTAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA
 AGGGCCGACA GGATTCAGG AGTCCTGAGA TGAGGGAGTC GTCCACCCAC TGACAGGGA GATCGTCGAA CCCGTGGGTC TGGATGTAGA CGTTGCACCT
 192 P A V L Q S S G L Y S L S S V V T V P S S S L G T Q T Y I C N V N
 1601 TCACAAGCCC AGCAACACCA AGGTGGACAA GAAAGTTGAG CCAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC CAGCACCTGA ACTCCTGGGG
 AGTGTTCGGG TCGTGTGGT TCCACCTGTT CTTTCAACTC GGGTTTAGAA CACTGTTTGG AGTGTGTACG GGTGGCAGG GTCTGTGGACT TGAGGACCCC
 225 H K P S N T K V D K K V E P K S C D K T H T C P P C P A P E L L G

FIG. 34B

1701 GGACCGTCAG TCCTCTCTTT CCCCCCAAAA CCCAAGGACA CCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT GGTGGACGTG AGCACAAG
 CCTGGCAGTC AGAAGGAGAA GGGGGGTTTT GGGTTCTCTGT GGAGTACTA GAGGGCTGG GGAATCCAGT GTACGCACCA CCACCTGCAC TCGGTGCTTC
 258 G P S V F L F P P K P K D T L M I S R T P E V T C V V V D V S H E D
 1801 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGA GGTGCATAAT GCCAAGACAA AGCCGGGGGA GGAGCAGTAC AACAGCACGT ACCGGGTGGT
 TGGGACTCCA GTTCAAGTTG ACCATGCACC TGCCGCACCT CCACGTATTA CGGTTCTGTT TCGGGCCCTT CCTCGTCATG TTGTCGTGCA TGGCCCAACA
 292 P E V K F N W Y V D G V E V H N A K T K P R E E Q Y N S T Y R V V
 1901 CAGCGTCTC ACCGTCTCTG ACCAGGACTG GCTGAATGGC AAGGAGTACA AGTCAAGGT CTCCAACAAA GCCCTCCAG CCCCACCGA GAAAACCATC
 GTCCGAGGAG TGGCAGGAG TGCTCTGAC CGACTTACCG TTCTCTCATGT TCACGTTCCTA GAGGTGTTT CCGGAGGCTC GGGGTAGCT CTTTGTGTAG
 325 S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I
 2001 TCCAAAGCCA AAGGCGAGC CCGAGAACA CAGGTGTACA CCTGCCCCC ATCCCGGGA GAGATGACCA AGAACAGGT CAGCCTGACC TGCTGTGCA
 AGTTTCTGGT TTCCCGTCCG GGCTCTTGGT GTCCACATGT GGGACGGGG TAGGGCCCTT CTCTACTGGT TCTTGGTCCA GTGGACTGG ACGGACAGT
 358 S K A K G Q P R E P Q V Y T L P P S R E E M T K N Q V S L T C L V K
 2101 AAGGCTCTA TCCAGCGAC ATCGCCGTGG AGTGGGAG CATTGGGCAG CCGGAGAACA ACTACAGAC CACGCCCTCC GTGCTGGACT CCGACGGCTC
 TTCCGAAGAT AGGTGCTGTG TAGCGGCACC TCACCTCTC GTTACCCGTC GGCTCTTGT TGAATGTTCTG GTGCGGAGG CACGACCTGA GGCTGCCGAG
 392 G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S
 2201 CTCTCTCTC TACAGCAAGC TCACCGTGA CAAGAGCAGG TGGCAGCAGG GGAAGTCTT CTCATGCTCC GTGATGCAAG AGGCTCTGCA CAACCACTAC
 GAAGAAGGAG ATGTCGTTG AGTGGCACCT GTTCTCGTCC ACCGTCGTC CCTTGCAGAA GAGTACGAGG CACTACGTAC TCCGAGACGT GTTGTGTATG
 425 F F L Y S K L T V D K S R W Q Q G N V F S C S V M H E A L H N H Y
 2301 ACGCAGAGA GCCTCTCCCT GTCTCCGGGT AAATGAGTGC GACGGCCCTA GATCGACCT GCAGAAGCTT GGCCGCCATG GCCCAACTTG TTTATTGCA
 TGCGTCTCT CCGAGAGGGA CAGAGGCCCA TTTACTCAGG CTGCGGGGAT CTCAGCTGGA CGTCTTCGAA CCGCGGGTAC CCGGTGGAAC AAATAACGTC
 458 T Q K S L S L S P G K O
 2401 CTTATAATGG TTACAAATAA AGCAATAGCA TCACAAATTT CACAAATAAA GCATTTTTTT CACTGCATTC TAGTTGTGGT TTGTCCAAAC TCATCAATGT
 GAATATTACC AATGTTTATT TCGTTATCGT AGTGTATAA GTGTTTATTT CGTAAAAAAA GTGACGTAAG ATCAACACCA AACAGGTTTG AGTAGTTACA

FIG. 34c

2501 ATCTTATCAT GTCTGGATCG ATCGGGAATT AATTCGGCGC AGCACCATGG CCTGAATAAA CCTCTGAAG AGGAACATTGG TTAGGTACCT TCTGAGGCGG
 TAGAATAGTA CAGACCTAGC TAGCCCTTAA TTAAGCCGCG TCGTGGTACC GGACTTTATT GGAGACTTTC TCCTTGAACC AATCCATGGA AGACTCCGCC
 2601 AAAGAACCAT CTGTGGGAATG TGTGTAGTT AGGGTGTGA AAGTCCCCAG GCTCCCCCAG AGGAGAGAT ATGCAAAAGCA TGCATCTCAA TTAGTCAGCA
 TTTCTTGGTA GACACCTTAC ACACAGTCAA TCCACACCTT TTAGGGGTC CGAGGGTTC TCCGTCTTCA TACGTTTCTT ACGTAGAGTT AATCAGTCGT
 2701 ACCAGGTGTG GAAGTCCCC AGGCTCCCCA GCAGGCAGAA GTATGCAAG CATGCATCTC AATTAGTCAG CAACCAATAGT CCGGCCCTTA ACTCCGCCCA
 TGGTCCACAC CTTTCAGGG TCCGAGGGT CGTCCGTCTT CATACGTTTC GTACGTAGAG TTAATCAGTC GTTGTATCA GGGCGGGGAT TGAGCGGGGT
 2801 TCCCGCCCCCT AACTCCGCC AGTTCGCCCC ATCTCCGCC CCATGGCTGA CTAATTTTTT TTATTTATGC AGAGGCGGAG GCCGCCTCGG CCTCTGAGCT
 AGGGCGGGGA TTGAGGCGGG TCAAGGCGGG TAAGAGCGGG GGTACCGACT GATTAAAAA AATAAATACG TCTCCGGCTC CGGCGGAGCC GGAGACTCGA
 2901 ATTCCAGAAG TAGTGAGGAG GCTTTTGTGG AGGCCTAGGC TTTTGCAAA AGCTGTAAAC AGCTTGGCAC TGGCCGTCTG TTTTACAACGT CGTGACTGGG
 TAAGGTCTTC ATCACTCCTC CGAAAAACC TCCGGATCCG AAAACGTTTT TCGACAATTG TCGAACCGTG ACCGGCAGCA AATGTGTGA GCACGTGACC
 3001 AAAACCCCTGG CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCCTTC GCCAGTTGGC GTAATAGCGA AGAGGCCCGC ACCGATCGCC CTTCCCAACA
 TTTTGGGACC GCAATGGGTT GAATTAGCGG AACGTCGTGT AGGGGGAAG CGGTCAACCG CATTTATCGCT TCTCCGGGCG TGGCTAGCGG GAAGGTTGT
 3101 GTTGGGTAGC CTGAATGGCG AATGGCGCCT GATCGGGTAT TTTCTCTCTTA CGCATCTGTG CGGTATTTCA CACCGCATAC GTCAAAGCAA CCATAGTACG
 CAACGCATCG GACTTACCGC TTACCGCGGA CTACGCCATA AAAGAGGAAT GCGTAGACAC GCCATAAAGT GTGGCGTATG CAGTTTCTGT GTATCATGC
 3201 CGCCCTGTAG CGGCGCATTA AGCGGGCGG GTGTGGTGGT TAGCGGCAGC GTGACCGCTA CACTTGGCAG CGCCCTAGCG CCCGCTCCTT TCGCTTTCTT
 GCGGGACATC GCCGCGTAAT TCGCGCCGCC CACACCACA ATGCGGTCTG CACTGGCGAT GTGAACGGTC GCGGATCGC GGGCGAGGAA AGCGAAAGAA
 3301 CCTTCTCTTT CTGCGCACGT TCGCCGGGTT TCCCGGTCAA GCTCTAAATC GGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC
 GGAAGGAAA GAGCGGTGCA AGCGGCCGAA AGGGGCAGTT CGAGATTAG CCCCCGAGG AATPCCCAAG GCTAATCAC GAAATGCCGT GGAGCTGGGG
 3401 AAAAAACTTG ATTTGGGTGA TGGTTACGT AGTGGGCCAT CGCCCTGATA GACGGTTTTT CGCCCTTGA CGTGGAGTC CACGTTCTTT AATAGTGGAC
 TTTTGTGAAC TAAACCCACT ACCAATGCA TCACCCGGTA CCGGGACTAT CTGCCAAAAA GCGGGAAACT GCACTCAG GTGCAAGAAA TTATCACCTG

FIG. 34 D

3501 TCTTGTTCAC AACTGGAACA ACACTCAACC CTATCTCGGG CTATTCTTTT GATTATTAAG GGATTTTGCC GATTTCCGCC TATTGGTTAA AAAATGAGCT
 AGAACAAAGGT TTGACCTTGT TGTGAGTTGG GATAGAGCCC GATAAGAAAA CTAAATATTC CTAAAGCCGG CTAAAGCCGG ATAACCAATT TTTTACTCGA

 3601 GATTTAACAA AAATTTTAACG CGAATTTTAA CAAAATATTA AGTTTACAA TTTTATGTTG CACTCTCAGT ACAATCTGCT CTGATGCCGC ATAGTTAAGC
 CTAATAATGTT TTTAAATTCG GCTTAAATTT GTTTTATAAT TGCATAATGTT AAAATACCAC GTGAGAGTCA TGTTAGACGA GACTACGGCG TATCAATTCG

 3701 CAACTCCGCT ATCGCTACGT GACTGGGTCA TGGCTGGCC CCGACACCCG CCAACACCCG CTGACGGGCT TGTCTGCTCC CGGCATCCGC
 GTTGAGCGCA TAGCGATGCA CTGACCCAGT ACCGACGCGG GGCTGTGGGC GGTGTGGGC GACTGCGCGG GACTGCCCGA ACAGACGAGG GCCGTAGGCG

 3801 TTACAGACAA GCTGTGACCG TCTCCGGGAG CTGCATGTGT CAGAGGTTTT CACCGTCATC ACCGAAACGC GCGAGGCGAT ATTCTTGAAG ACGAAAGGC
 AATGCTCTGTT CGACACTGGC AGAGGCCCTC GACGTACACA GTCTCCAAA GTGCGAGTAG TGGCTTTGCG CGCTCCGTCA TAAGAACATC TGCCTTCCCC

 3901 CTCGTGATAC GCTATTTTT ATAGGTTAAT GTCATGATAA TAATGGTTTC TTAGACGTCA GTTGGCACTT TTCGGGGAAA TGTGCGCGGA ACCCCTATTT
 GAGCACTATG CGGATAAAAA TATCCAATTA CAGTACTATT ATTACCAAG AATCTGCAGT CCACCGTGAA AAGCCCTTT ACACGCGCCT TGGGGATAAA

 4001 GTTTATTTTT CTAAATACAT TCAAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA TGCTTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTC
 CAAATAAAAA GATTATGTA AGTTATACA TAGGCGAGTA CTCTGTTATT GGGACTATTT ACGAAGTTAT TATAACTTTT TCCTTCTCAT ACTCATAGT

 4101 ACATTTCCGT GTCGCCCCTA TTCCCTTTTT TCGGGCATTT TGCCCTTCTG CCCAGAAAAC CTGGTGAAAG TAAAAGATGC TGAAGATCAG
 TGTAAAGGCA CAGCGGGGAT AAGGAAAAA ACGCGTAAA ACGGAAGGAC AAAAACGAGT GGGTCTTTGC GACCACCTTC ATTTTCTACG ACTTCTAGTC

 4201 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG AAGAACGTTT TCCAATGATG AGCACTTTTA
 AACCACGTG CTCACCCAAT GTAGCTTGAC CTAGAGTTGT CGCCATTCTA GGAACCTCTA AAAGCGGGGC TTCTTGCAAA AGGTTACTAC TCGTGAATAA

 4301 AAGTCTGCT ATGTGGCGCG GTATTATCCC GTGATGACGC CCGGCAAGAG CAACTCGGTC GCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC
 TTCAAGACGA TACACCGCGC CATAATAGG CACTACTGCG GCCCGTTCTC GTTGAGCCAG CGGCTATGT GATAAGAGTC TTACTGAACC AACTCATGAG

 1401 ACCAGTCACA GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGTCTG CATAACCATG AGTGATAACA CTGCGGCCAA CTTACTTCTG
 TGGTCACTGT CTTTTCGTAG AATGCTTACC GTACTGTGAT TCTCTTAATA CGTCAGAGG GTATTGGTAC TCATATTGT GACGCGGTT GAATGAAGAC

 1501 ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTTC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGA ACCGAGCTG AATGAAGCA
 TGTGTGCTAG CTCCTGGCTT CCTCGATGG CGAAAAACG TGTGTATACC CCTAGTACAT TGAGCGGAAC TAGCAACCT TGCCCTCGAC TTACTTCTGCT

FIG. 34E

4601 TACCAAAACGA CGAGCGGTGAC ACCACGATGC CAGCAGCAAT GGCACAACAG TTGGCGAAAC TATTAACCTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA
 ATGGTTTGCT GCTCGCACTG TGGTGCTAGC GTGCTCGTTA CCGTTCTGC AACCGTTTG ATAATTGACC GCTTGATGAA TGAGATCGAA GGGCCGTTGT
 4701 ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCCTCGCT CGGCCCTTCC GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCGGGTGAG
 TAATTATCTG ACCTACCTCC GCCTATTTCA AGTCTCTGGT GAAGACCGGA GCCGGGAAGG CCGACCGAGC AAATAACGAC TATTAGACC TCGGCCACTC
 4801 CGTGGGTCTC GGGTATCAT TGCAGCACTG GGGCCAGATG GTAAGCCCTC CCGATCTGTA GTTATCTACA CGACGGGAG TCAGGCAACT ATGGATGAAC
 GCACCCAGAG CGCCATAGTA ACGTCGTGAC CCGGTCTAC CATTCGGGAG GGCATAGCAT CAATAGATGT GCTGCCCTC AGTCCGTTGA TACCTACTTG
 4901 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTACTC ATATATACTT TAGATTGATT TAAAACTTCA
 CTTTATCTGT CTAGCGACTC TATCCACGGA GTGACTTAAT CGTAACCAAT GACAGTCTGG TTCAAATGAG TATATATGAA ATCTAATAA ATTTTGAAGT
 5001 TTTTAAATTT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT AATCTCAUGA CCAAAATCCC TTAACGTGAG TTTTCGTTC ACTGAGCGTC AGACCCCGTA
 AAAAATTAAA TTTTCTCTAGA TCCACTCTTA GGAAAACTA TTAGAGTACT GGTTTTAGG AATTGCACCT AAAAGCAAGG TGACTCCGAG TCTGGGGCAT
 5101 GAAAAGATCA AAGGATCTTC TTGAGATCCT TTTTCTCTGC GCGTAATCTG CTGCTTGCAA AAAAAAAC CACCGCTACC AGCGTGGTT TGTTCGCCG
 CTTTCTTAGT TTCTTAGAAG AACTCTAGGA AAAAAGACG CGCATTAGAC GACGAACGTT TGTTTTGTG GTGGCGATGG TCGCCACCAA ACAAAACGGC
 5201 ATCAAGAGCT ACCAATCTT TTTCCGAAG TAACTGGCTT CAGCAGAGCG CAGATACCAA ATACTGTCTT TCTAGTGATG CCGTAGTTAG GCCACCACTT
 TAGTTCTCGA TGGTTGAGAA AAAGGCTTCC ATTGACCGAA GTGCTCTCGC GTCTATGGTT TATGACAGGA AGATCACATC GGCATCAATC CCGTGGTGAA
 5301 CAAGAAGTCT GTAGCACCGC CTACATACCT CGCTCTGCTA ATCTGTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTGT GTCTTACCGG GTTGGACTCA
 GTTCTTGAGA CATCGTGGCG GATGTATGGA GCGAGACGAT TAGGACAATG GTCACCGACG ACGTCAACG CTATTACGA CAGAATGGCC CAACCTGAGT
 5401 AGACGATAGT TACCGGATAA GGGCAGCGG TCGGGCTGAA CCGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC
 TCTGCTATCA ATGGCCTATT CCGGTCGCC AGCCCGACTT GCCCCCCAAG CAGGTGTGTC GGGTCGAACC TCGTGTGCTG GATGTGGCTT GACTCTATGG
 5501 TACACCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGCGG GACAGGTATC CGGTAAGCGG CAGGTCGGA ACAGGAGAGC GCACGAGGGA
 ATGTGCACT CGTAATCTT TCGCGGTGCG AAGGGCTTCC CTCCTTCCG CTTCTCCATAG GCCATTGCC GTCCAGCCT TGTCTCTCTCG CGTGTCTCTT
 601 GCTTCCAGG GGAACGGCT GGTATCTTTA TAGTCTGTC GGGTTTCGCC ACCCTGACT TGAGCGTCA TTTTGTGTAT GCTCGTCAGG GGGCGGAGC
 CGAAGGTCCC CCTTTCGGA CCATAGAAAT ATCAGGACAG CCCAAAGCGG TGGAGACTGA ACTCGCAGT AAAAACACTA CGAGCAGTCC CCCCCTCTCG

FIG. 34 F

5701 CTATGGGAAA ACGCCAGCAA CGCGGCCCTTT TTACCGTTCC TGGCCCTTTG CTGGCCCTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG
GATACCTTTT TCGCGTCGTT GCGCCGAAA AATGCCAAGG ACCGGAAAAC GACCGGAAA CGAGTGACA AGAAGGACG CAATAGGGA CTAAGACACC

5801 ATAAACGTAT TACCGCCCTTT GAGTGAGTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG GAAGCGGAAG AGCGCCCAAT
TATTGGCATA ATGGCGGAAA CTCACTCGAC TATGGCGAGC GCGCTCGGCT TGCTGGCTCG CGTCGCTCAG TCACTCGCTC CTTCGCCCTC TCGCGGGTTA

5901 ACGCAAACCG CCTCTCCCG CGCGTTGGCC GATTCATTAA TCCAACTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT
TGCGTTTGGC GGAGAGGGGC GCGCAACCG CTAAGTAATT AGGTTGACCG TGCTGTCCAA AGGCTGACC TTTCGCCCGT CACTCGCGTT GCGTTAATTA

6001 GTGAGTTACC TCACTCATTG GGCACCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT CACACAGGAA
CACTCAATGG AGTGAGTAAT CCGTGGGCTC CGAAATGTGA AATACGAAG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA GTGTGTCCCTT

6101 ACAGCTATGA CCATGATTAC GAATTA
TGTCGATACT GGTACTAATG CTTAAT

FIG. 34

LC Frequency																	
28	S	511	N	V	D	G	I	T	L	X							
29	I	612	S	V	G	N	X		16	35							
30	S	849	N	K	G	R	Y	T	D	A	X						
31	S	676	N	T	R	I	D	K	G	X							
32	Y	1055	N	W	F	S	D	R	X								
50	G	386	A	D	W	K	L	E	S	X							
53	S	545	N	T	K	I	R	X	30	82							
91	Y	849	S	R	A	G	H	X									
92	Y	362	G	N	S	D	L	T	H	I	X						
93	S	738	N	Q	T	H	G	D	R	X							
94	S	386	T	W	Y	L	F	A	P	V							
96	L	264	Y	W	F	I	R	P	X								

FIG. 35

Residue	Natural Diversity	Diversity < DNA codon	% good	% covering
L1-28	SNVDGI	SNVDGI<RDT>	100%	94%
L1-29	ISVGN	ISVG<RKT>	100%	86%
L1-29		IV<RTT>	100%	56%
L1-30	SNKGRYTDA	SNKGGRTTDAAE<RVW>	92%	93%
L1-31	SNTRIDKG	SNTRDKGGAAE<RVW>	75%	95%
L1-31		SNTTRIHK<ANW>	100%	94%
L1-32	YNWFSDR	YNFSDATIV<DHT>	55%	88%
L1-32		YFS<THT>	100%	77%
L2-50	GADWKLES	GAWLSV<KBG>	83%	67%
L2-53	SNTKIR	SNT<AVC>	100%	90%
L3-91	YSRAGH	YSAD<KMT>	75%	74%
		YS<TMT>	100%	66%
L3-92	YGNSDLTHI	YNSDTIFAV<DHT>	67%	64%
		YNSDTA<DMC>	83%	62%
L3-93	SNQTHGDR	SNTGDA<RVT>	83%	80%
		SNTDYAFIV<DHT>	44%	76%
L3-94	STWYLFAPVI	STYLFAPVINDH<NHT>	75%	78%
		STYFIN<WHT>	83%	43%
L3-96	LYWFIRP	LYFPHS<YHT>	67%	52%
		LYFIHN<HWT>	67%	58%
		LFI<HTT>	100%	42%
		LLWR<YKG>	100%	47%
		YF<TWT>	100%	29%

FIG. 36

Light Chain Designed Diversity
Diversity: $\sim 2.9 \times 10^9$

CDR-L1: diversity $\sim 7 \times 10^3$

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		R	R	V
				Y

CDR-L2: diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity $\sim 2.3 \times 10^4$

91	92	93	94	96
KMT	DHT	DHT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	F	F	F	L
Y	I	I	H	P
	N	N	I	S
	S	S	L	Y
	T	T	N	
	V	V	P	
	Y	Y	S	
			T	
			V	
			V	
			Y	

FIG. 37

Light Chain Designed Diversity
Diversity: $\sim 6.1 \times 10^8$

CDR-L1: diversity $\sim 3.4 \times 10^3$

28	29	30	31	32
RDT	RTT	RVW	ANW	THT
D	I	D	I	F
G	V	E	K	S
I		G	N	Y
N		K	R	
S		N	S	
V		S	T	
		T		
		V		

CDR-L2: diversity = 18

50	53
KBG	AVC
A	N
G	S
L	T
S	
V	
W	

CDR-L3: diversity $\sim 1.0 \times 10^4$

91	92	93	94	96
KMT	DMC	RVT	NHT	YHT
A	A	A	A	F
D	D	D	D	H
S	N	G	F	L
Y	S	N	H	P
	T	S	I	S
	Y	T	L	Y
			N	
			P	
			S	
			T	
			V	
			Y	

FIG. 38

Light Chain Designed Diversity**CDR-L3: diversity $\sim 1.3 \times 10^3$**

91	92	93	94	96
TMT	DMC	RVT	WHT	HTT
S	A	A	F	F
Y	D	D	I	I
	N	G	N	L
	S	N	S	
	T	S	T	
	Y	T	Y	

FIG. 39**CDR-L1**

28	29	30	31	32
RDT	RTT	RVW	RVW	DHT
D	I	D	D	A
G	V	E	E	D
I		G	G	F
N		K	K	I
S		N	N	N
V		S	S	S
		T	T	T
		V	V	V
				Y

CDR-L2

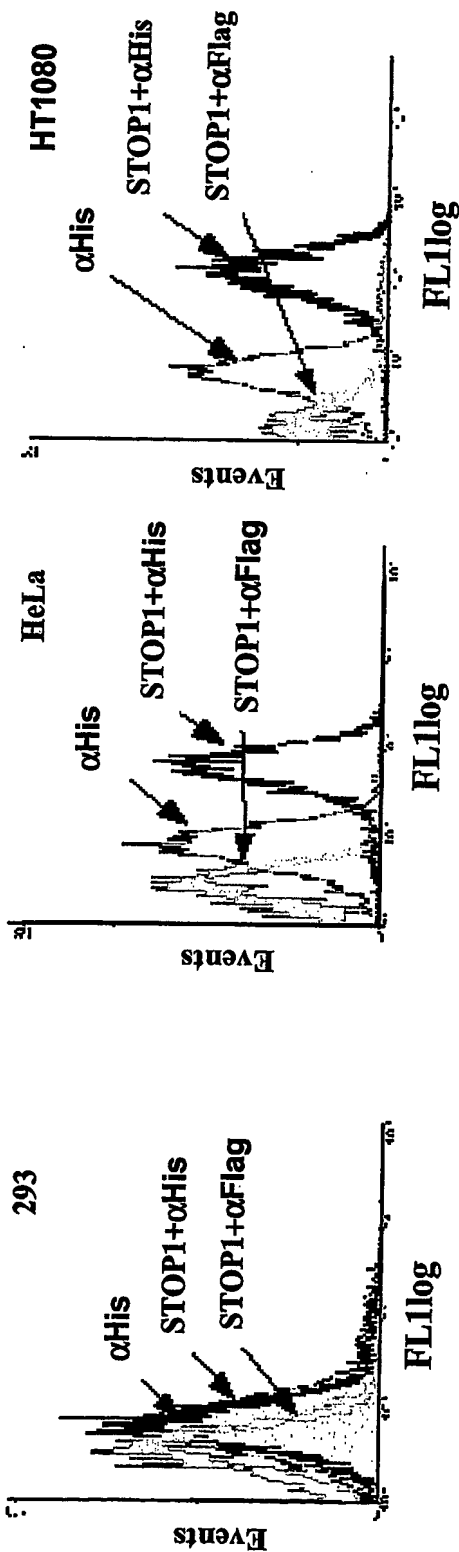
50	53
DVK	AVM
A	N
G	K
L	R
S	S
V	T2
W	

CDR-L3

91	92	93	94	96
NRT	NRT	RVM	NNK	TDK
C	C	A2	A	C
D	D	D	C	F
G	G	E	D	L
H	H	G2	E	W
N	N	K	F	Y
R	R	N	G	*
S	S	R	H	
Y	Y	S	I	
		T2	L	
			M	
			N	
			P	
			Q	
			R	
			etc	
			*	

*Amber stop codon is encoded by the degenerate codon

FIG. 40



HUVEC

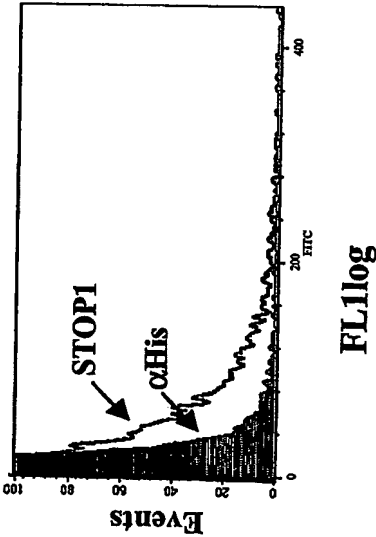


FIG.41

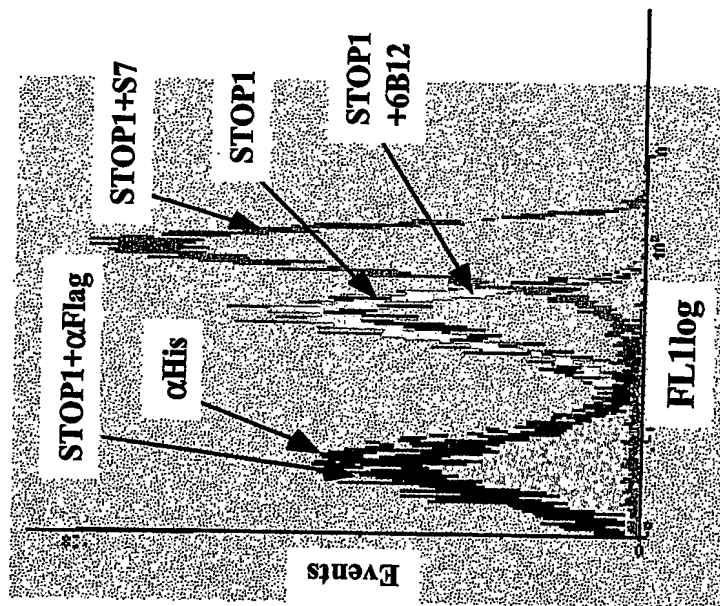
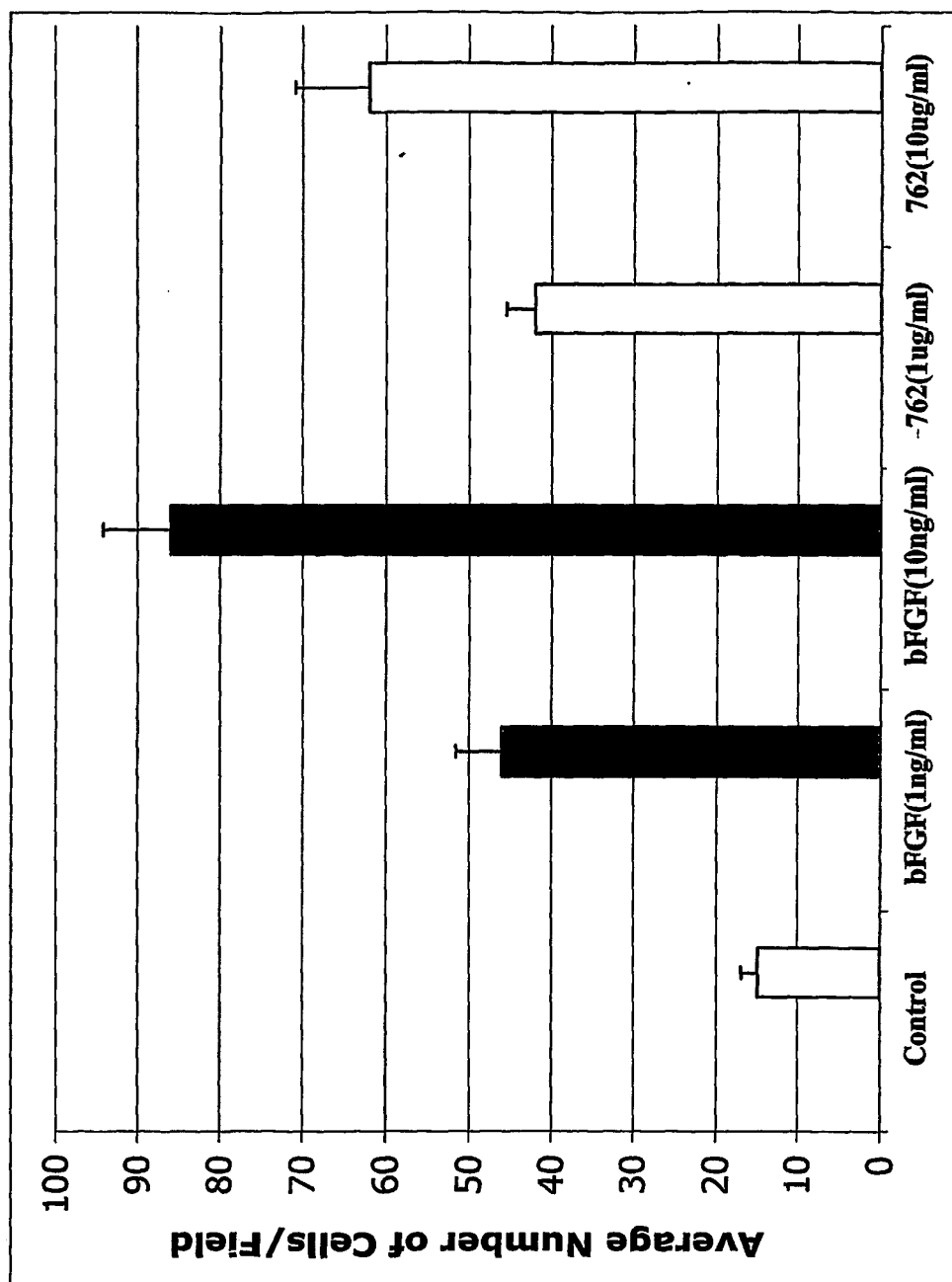
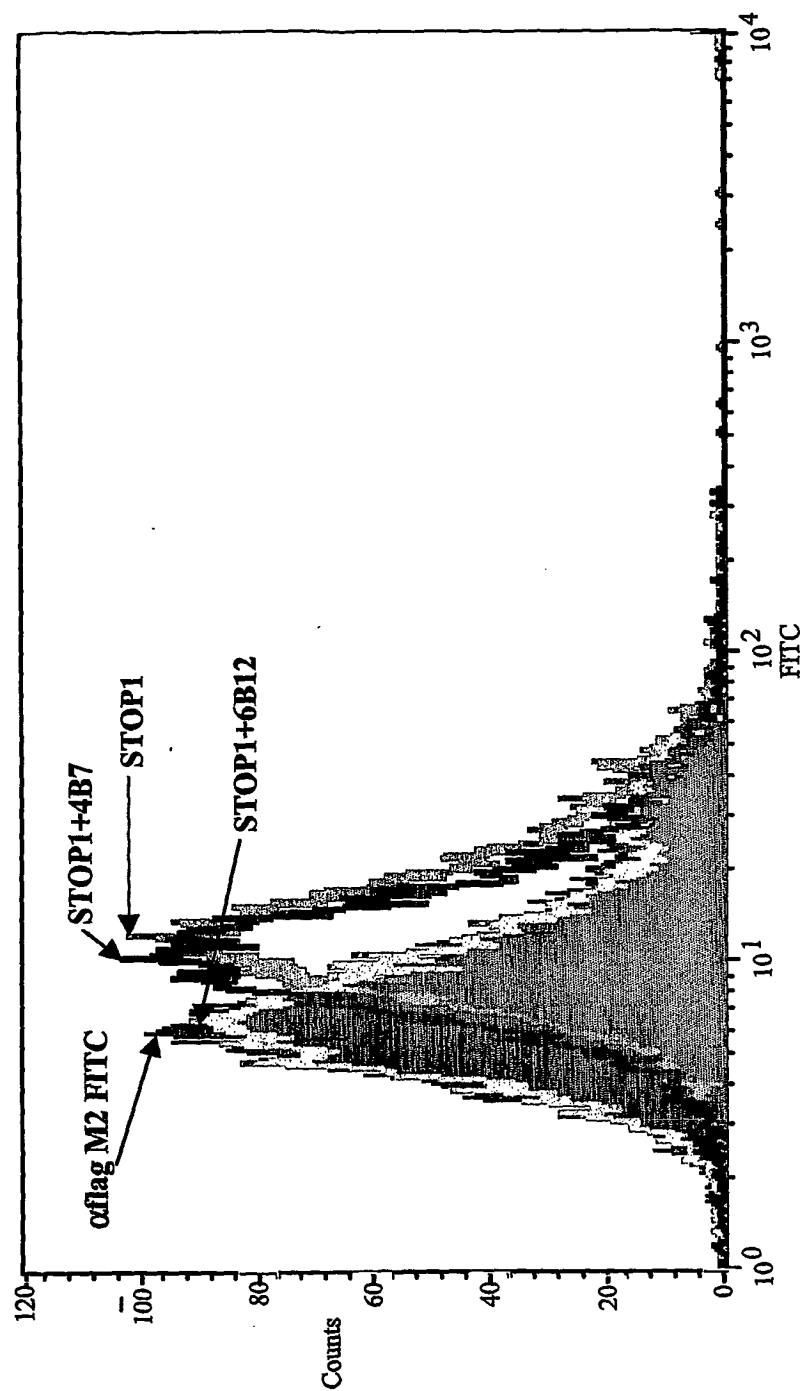
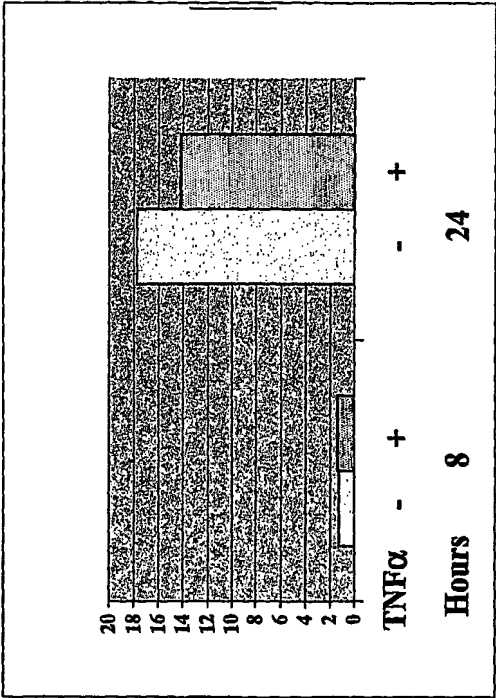


FIG.42

**FIG.43**

**FIG.44**

A.



B.

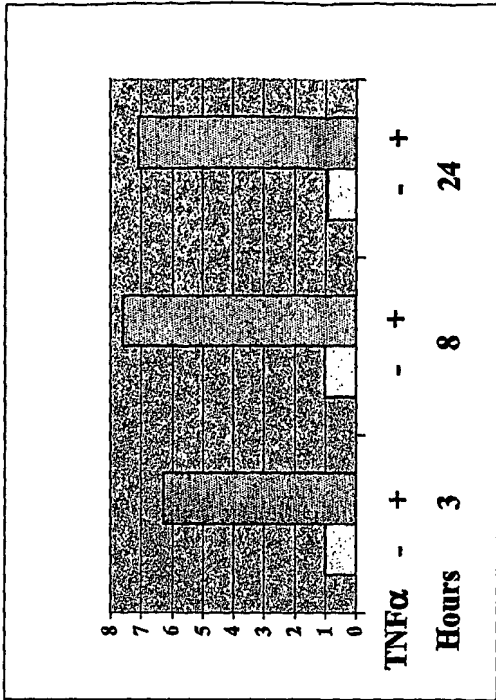


FIG.45

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